

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.2326 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	Nan	1 2	ADD95004	Add95004 Platelet
2	0	Nan	1 2	ADD94992	Add94992 Platelet
3	0	Nan	1 2	ADD94993	Add94993 Platelet
4	0	Nan	1 2	ADD95002	Add95002 Platelet
5	0	Nan	1 2	ADD94997	Add94997 Platelet
6	0	Nan	1 2	ADD94999	Add94999 Platelet
7	0	Nan	1 2	ADD95003	Add95003 Platelet
8	0	Nan	1 2	ADD94995	Add94995 Platelet
9	0	Nan	1 2	ADD94998	Add94998 Platelet
10	0	Nan	1 2	ADD95001	Add95001 Platelet
11	0	Nan	1 2	ADD94990	Add94990 Platelet
12	0	Nan	1 2	ADD94991	Add94991 Platelet
13	0	Nan	1 2	ADD94994	Add94994 Platelet
14	0	Nan	1 2	ADD94996	Add94996 Platelet
15	0	Nan	1 2	ADD95000	Add95000 Platelet
16	0	Nan	1 2	AAY46652	Aay46652 Immunogen
17	0	Nan	1 4	AAM97834	Aam97834 Human pep
18	0	Nan	1 4	AAM97974	Aam97974 Human pep
19	0	Nan	1 4	AAM97643	Aam97643 Human pep
20	0	Nan	1 4	AAM98447	Aam98447 Human pep
21	0	Nan	1 4	AAM98354	Aam98354 Human pep
22	0	Nan	1 4	AAM53290	Aam53290 Human non
23	0	Nan	1 4	AAM53329	Aam53329 Human non
24	0	Nan	1 4	AAM53291	Aam53291 Human non

25	0	Nan	1 4	AAM53328	Aam53328 Human non
26	0	Nan	1 4	AAM53219	Aam53219 Human non
27	0	Nan	1 4	AAM53218	Aam53218 Human non
28	0	Nan	1 4	AAB91029	Aab91029 Thyrotrop
29	0	Nan	1 4	AAB91739	Aab91739 Opioid pe
30	0	Nan	1 4	AAB92150	Aab92150 Polypepti
31	0	Nan	1 4	AAB91892	Aab91892 Apoptosis
32	0	Nan	1 4	AAB91546	Aab91546 Endotheli
33	0	Nan	1 4	AAB92392	Aab92392 Miscellan
34	0	Nan	1 4	AAB91665	Aab91665 Opioid pe
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ALIGNMENTS

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ADD95004
ID ADD95004 standard; peptide; 1 AA.
XX AC ADD95004;
XX DT 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #146.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "OTHER= H2NC (=NH) NH (CH2) CO. Beta-Ala (not defined)"
XX PN WO9501371-A1.
XX PD 12-JAN-1995.
XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX DR WPI; 1995-060950/08.
XX PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain
XX FT guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 11; 34pp; Japanese.
XX CC The invention describes peptides of amino acid sequence (I) and their
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or
XX CC amidino group, (I) are provided with excellent stability so that their
XX CC activity can be exhibited for an effective time after administration.
XX CC Thereafter they are readily metabolised and expelled. This is the amino
XX CC acid sequence of a platelet aggregation inhibitor peptide.

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Query Match      NaN%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 R 1

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AC ADD94992;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #134.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
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FH Key Location/Qualifiers
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FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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PN WO9501371-A1.
XX
PD 12-JAN-1995.
XX
PF 22-JUN-1994; 94WO-JP000999.
XX
PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA ) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
PI WPI; 1995-060950/08.
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PS Disclosure; Page 10; 34pp; Japanese.
XX
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CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
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SQ Sequence 1 AA;
Query Match      NaN%; Score 0; DB 2; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1

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ID ADD94993 standard; peptide; 1 AA.
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AC ADD94993;
XX
DT 29-JAN-2004 (first entry)
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XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
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FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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PN WO9501371-A1.
XX
PD 12-JAN-1995.
XX
PF 22-JUN-1994; 94WO-JP000999.
XX
PR 30-JUN-1993; 93JP-00186755.
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CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
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SQ Sequence 1 AA;
Query Match      NaN%; Score 0; DB 2; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1

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ADD95002
ID ADD95002 standard; peptide; 1 AA.
XX
AC ADD95002;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #144.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

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AC ADD95003;
XX
DT 29-JAN-2004 (first entry)
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KW platelet aggregation inhibitor; guanidino group; amidino group.
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OS Unidentified.
XX
FH Key Location/Qualifiers
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FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
XX
PN WO9501371-A1.
XX
PD 12-JAN-1995.
XX
PF 22-JUN-1994; 94WO-JP0000999.
XX
PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
DR WPI; 1995-060950/08.
XX
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
PS Disclosure; Page 11; 34pp; Japanese.
XX
CC The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match NaN%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

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XX
AC ADD94995;
XX

DT 29-JAN-2004 (first entry)
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DE Platelet aggregation inhibitor peptide #137.
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KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
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FH Key Location/Qualifiers
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
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PN WO9501371-A1.
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PD 12-JAN-1995.
XX
PF 22-JUN-1994; 94WO-JP0000999.
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PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
DR WPI; 1995-060950/08.
XX
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
PS Disclosure; Page 10; 34pp; Japanese.
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CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match NaN%; Score 0; DB 2; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

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ID ADD94998 standard; peptide; 1 AA.
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AC ADD94998;
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DT 29-JAN-2004 (first entry)
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KW platelet aggregation inhibitor; guanidino group; amidino group.
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OS Unidentified.
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FH Key Location/Qualifiers
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"
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PN WO9501371-A1.

XX 12-JAN-1995.
XX
XX 22-JUN-1994; 94WO-JP0000999.
XX
XX 30-JUN-1993; 93JP-00186755.
XX
XX (YAWA) NIPPON STEEL CORP.
XX
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
XX Disclosure; Page 10; 34pp; Japanese.
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XX The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

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XX AC ADD95001;
XX
XX 29-JAN-2004 (first entry)
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XX
XX platelet aggregation inhibitor; guanidino group; amidino group.
XX
XX Unidentified.
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XX Key Location/Qualifiers
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FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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XX WO9501371-A1.
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XX 12-JAN-1995.
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XX 12-JAN-1995.
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XX 22-JUN-1994; 94WO-JP0000999.
XX
XX 30-JUN-1993; 93JP-00186755.
XX
XX (YAWA) NIPPON STEEL CORP.
XX
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.

XX Disclosure; Page 10; 34pp; Japanese.
XX
XX The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
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Query Match NaN; Score 0; DB 2; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

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XX 22-JUN-1994; 94WO-JP0000999.
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XX 30-JUN-1993; 93JP-00186755.
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XX (YAWA) NIPPON STEEL CORP.
XX
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
XX Disclosure; Page 10; 34pp; Japanese.
XX
XX The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
XX Sequence 1 AA;
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Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

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AC ADD94991;
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DT 29-JAN-2004 (first entry)
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XX
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OS Unidentified.
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PF 22-JUN-1994; 94WO-JP0000999.
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PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
DR WPI; 1995-060950/08.
XX
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
PS Disclosure; Page 10; 34pp; Japanese.
XX
CC The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 13
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ID ADD94994 standard; peptide; 1 AA.
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AC ADD94994;
XX
DT 29-JAN-2004 (first entry)
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DE Platelet aggregation inhibitor peptide #136.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
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OS Unidentified.
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FH Key Location/Qualifiers
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PN WO9501371-A1.
XX
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XX
PF 22-JUN-1994; 94WO-JP0000999.
XX
PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
DR WPI; 1995-060950/08.
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XX
PS Disclosure; Page 10; 34pp; Japanese.
XX
CC The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;

Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

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AC ADD94996;
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DT 29-JAN-2004 (first entry)
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KW platelet aggregation inhibitor; guanidino group; amidino group.
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FH Key Location/Qualifiers
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PN WO9501371-A1.
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PD 12-JAN-1995.

XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX DR
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX PT guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.
XX CC The invention describes peptides of amino acid sequence (I) and their
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or
XX CC amidino group, (I) are provided with excellent stability so that their
XX CC activity can be exhibited for an effective time after administration.
XX CC Thereafter they are readily metabolised and expelled. This is the amino
XX CC acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;
Query Match NaN; Score 0; DB 2; Length 1;
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 R 1
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XX AC ADD95000;
XX DT 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #142.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
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XX PD 12-JAN-1995.
XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX DR
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX PT guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.

XX CC The invention describes peptides of amino acid sequence (I) and their
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or
XX CC amidino group, (I) are provided with excellent stability so that their
XX CC activity can be exhibited for an effective time after administration.
XX CC Thereafter they are readily metabolised and expelled. This is the amino
XX CC acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;
Query Match NaN; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 R 1
Search completed: May 2, 2006, 08:54:56
Job time : 91.2326 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 14.5116 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0

Sequence: 1 XXXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	Nan	3	3	A22565 R-phycoerythrin al
2	0	Nan	3	3	PQ0010 angiotensin-conver
3	0	Nan	3	3	S13894 histidinol dehydro
4	0	Nan	3	3	A43391 TRH-like tripeptid
5	0	Nan	3	3	E37196 bradykinin-potenti
6	0	Nan	3	3	F37196 bradykinin-potenti
7	0	Nan	3	3	I50412 gene p20K protein
8	0	Nan	3	3	PT0636 T-cell receptor be
9	0	Nan	3	3	PT0578 T-cell receptor be
10	0	Nan	3	3	PT0571 T-cell receptor be
11	0	Nan	3	3	PT0622 T-cell receptor be
12	0	Nan	3	3	I78890 tyrosine protein k
13	0	Nan	3	3	S68328 blood cell protein
14	0	Nan	3	3	T13892 cytochrome-c oxida
15	0	Nan	3	3	GKHU growth-modulating
16	0	Nan	3	3	RHPGT thyroliberin - pig
17	0	Nan	3	3	A60898 bursin - chicken
18	0	Nan	3	3	A23751 spinal cord peptid
19	0	Nan	3	3	B23751 spinal cord peptid
20	0	Nan	3	3	A33802 thyrotropin-releas
21	0	Nan	3	3	RHSHT thyroliberin - she
22	0	Nan	3	3	A92971 thyroliberin - eas
23	0	Nan	3	3	RHTDFO thyroliberin - Bom
24	0	Nan	4	1	ECXAA antho-Ramide neur
25	0	Nan	4	2	S18401 thyroglobulin - do
26	0	Nan	4	2	A02147 phagocytosis-stimu
27	0	Nan	4	2	A37832 phenol 2-monooxyge
28	0	Nan	4	2	A48360 gamma subunit of P
29	0	Nan	4	2	A61300 22K superhelical D

30	0	Nan	4	2	A41890 protein D - Escher
31	0	Nan	4	2	S43014 hypothetical prote
32	0	Nan	4	2	D41654 hypothetical prote
33	0	Nan	4	2	B43848 cell surface adhes
34	0	Nan	4	2	I40505 hypothetical prote
35	0	Nan	4	2	I40870 phospholipase C (E
36	0	Nan	4	2	T46627 hypothetical prote
37	0	Nan	4	2	S53508 starvation-induced
38	0	Nan	4	2	A27897 glucan 1,4-alpha-g
39	0	Nan	4	2	T30569 hypothetical prote
40	0	Nan	4	2	I38888 COI intron 16 prot
41	0	Nan	4	2	A25844 autho-RF amide neu
42	0	Nan	4	2	A34626 RPCH-related neuro
43	0	Nan	4	2	I51049 metallothionein-A
44	0	Nan	4	2	S39390 myosin-light-chain
45	0	Nan	4	2	I61883 protamine P1 - Ora

ALIGNMENTS

RESULT 1

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Molecule type: protein
A:Residues: 1-3 <KLO>
A:Cross-references: UNIPARC:UPI0000017CE9A

Query Match Nan%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 2 Y 2

RESULT 2

PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N:Alternate names: ficus latex peptide 3
C:Species: Ficus carica (common fig)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PQ0010
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0010
A:Molecule type: protein
A:Residues: 1-3 <MAR>
A:Cross-references: UNIPARC:UPI000011E971
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match Nan%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 L 1

RESULT 3

S13894
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S13894
R;Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: S13894; MUID:91112783; PMID:1989490
A;Accession: S13894
A;Molecule type: protein
A;Residues: 1-3 <NAG>
A;Cross-references: UNIPARC:UPI000017CE9B
A;Experimental source: var. capitata
C;Keywords: dimer; NAD; oxidoreductase

Query Match
Best Local Similarity NaN%; Score 0; DB 3; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 X 1

RESULT 4
A43391
TRH-like tripeptide - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
R;Lackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-
A;Reference number: A43391; MUID:92388092; PMID:1517203
A;Accession: A43391
A;Molecule type: protein
A;Residues: 1-3 <LAC>
A;Cross-references: UNIPARC:UPI000017CE9C
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match
Best Local Similarity NaN%; Score 0; DB 3; Length 3;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 5
E37196
bradykinin-potentiating peptide 5 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Accession: E37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: E37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <CIN>
A;Cross-references: UNIPARC:UPI0000158403
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity NaN%; Score 0; DB 3; Length 3;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 6
F37196
bradykinin-potentiating peptide 6 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: F37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: F37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <CIN>
A;Cross-references: UNIPARC:UPI000017CE9D
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity NaN%; Score 0; DB 3; Length 3;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 Q 1

RESULT 7
I50412
gene p20K protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: I50412
R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
J. Biol. Chem. 268, 8131-8139, 1993
A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicke
A;Reference number: A46643; MUID:93216790; PMID:8463325
A;Accession: I50412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3 <MAO>
A;Cross-references: UNIPARC:UPI00000618AB; GB:L02537; NID:g212616; PID:g212617
C;Genetics:
A;Gene: p20K

Query Match
Best Local Similarity NaN%; Score 0; DB 3; Length 3;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 2 S 2

RESULT 8
PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0636
A;Status: translation not shown
A;Molecule type: mRNA

A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9E
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 A 1

RESULT 9

PT0578
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0578
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0578
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CE9F
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 A 1

RESULT 10

PT0571
T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0571
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CEAO
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 A 1

RESULT 11

PT0622
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: PT0622; PT0680; PT0582; PT0673
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0622
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Cross-references: UNIPARC:UPI000017CEA1
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P

A;Accession: PT0680
A;Status: translation not shown
A;Molecule type: DNA

A;Residues: 1-3 <FEE1>

A;Cross-references: UNIPARC:UPI000017CEA1

A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F
A;Accession: PT0582

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-3 <FEE2>

A;Cross-references: UNIPARC:UPI000017CEA1

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A

C;Keywords: T-cell receptor

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 A 1

RESULT 12

I78890
tyrosine protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: I78890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, M.
Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntck, a csk-related tyrosine protein kinase.
A;Reference number: I58407; MUID:95060800; PMID:7970703

A;Accession: I78890

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3 <RES>

A;Cross-references: UNIPARC:UPI000011E834; GB:L33339; NID:G609536; PIDN:AAA64432.1; PII

C;Genetics:

A;Gene: p52ntk

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 3 T 3

RESULT 13

S68328
blood cell protein A - Molgula manhattensis (fragment)

C;Species: Molgula manhattensis

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: S68328

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68328

A;Molecule type: protein

A;Residues: 1-3 <TAY>
A;Cross-references: UNIPARC:UPI000017CEA2

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 A 1

RESULT 14

T13892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: UNIPARC:UPI000011E981; EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; F
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 2 T 2

RESULT 15

GKHU
growth-modulating peptide - human
C;Species: Homo sapiens (man)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Accession: A01421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
A;Accession: A01421
A;Molecule type: protein
A;Residues: 1-3 <SCH>
A;Cross-references: UNIPARC:UPI000012BB5C
A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inh

Query Match NaN%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 G 1

Search completed: May 2, 2006, 08:56:20
Job time : 15.5116 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.6047 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	Nan	2	1 GWA_SEPOF	P83570 sepia offic
2	0	Nan	3	1 GRWM_HUMAN	P01157 homo sapien
3	0	Nan	3	1 LUXE_VIBFI	P24272 vibrio fisc
4	0	Nan	3	1 THYL_BOMOR	P62970 bombina ori
5	0	Nan	3	1 THYL_NOTVI	P62971 notophthalm
6	0	Nan	3	1 THYL_PIG	P62968 sus scrofa
7	0	Nan	3	1 THYL_SHEEP	P62969 ovis aries
8	0	Nan	4	1 ACH1_ACHFU	P35904 achatina fu
9	0	Nan	4	1 DCML_PSECH	P19916 pseudomonas
10	0	Nan	4	1 DCMS_PSECH	P19918 pseudomonas
11	0	Nan	4	1 EOSI_HUMAN	P02731 homo sapien
12	0	Nan	4	1 FAR3_HIRME	P42562 hirudo medi
13	0	Nan	4	1 FAR4_HIRME	P42563 hirudo medi
14	0	Nan	4	1 FFKA_ATEL	P58705 anthopleura
15	0	Nan	4	1 FLRF_HELTI	P69138 helisoma tr
16	0	Nan	4	1 FLRF_HIRME	P69137 hirudo medi
17	0	Nan	4	1 FLRN_ATEL	P58707 anthopleura
18	0	Nan	4	1 FMRF_HELTI	P69148 helisoma tr
19	0	Nan	4	1 FMRF_HIRME	P69147 hirudo medi
20	0	Nan	4	1 FMRF_MACNI	P69145 macrocallis
21	0	Nan	4	1 FMRF_NERVI	P69146 nereis vire
22	0	Nan	4	1 FYRI_ATEL	P58706 anthopleura
23	0	Nan	4	1 ILME_SEPOF	P83568 sepia offic
24	0	Nan	4	1 OCP1_OCTMI	P58648 octopus min
25	0	Nan	4	1 OCP3_OCTMI	P58649 octopus min
26	0	Nan	4	1 TPAN1_PANIM	P84465 pandinus im
27	0	Nan	4	1 TPAN2_PANIM	P84464 pandinus im
28	0	Nan	4	1 TUFT_HUMAN	P01858 homo sapien
29	0	Nan	4	1 YLM1_YEAST	P36515 saccharomyc
30	0	Nan	4	2 Q16047_HUMAN	Q16047 homo sapien
31	0	Nan	4	2 Q96AT0_HUMAN	Q96at0 homo sapien

32	0	Nan	4	2 Q08433_9MURI	Q08433 rattus sp.
33	0	Nan	5	1 ALL14_CARMA	P81817 carcinus ma
34	0	Nan	5	1 AP21_EISFO	P84182 eisenia foe
35	0	Nan	5	1 BIOA_CITFR	P13071 citrobacter
36	0	Nan	5	1 BIOB_CITFR	P12997 citrobacter
37	0	Nan	5	1 BPP7_BOTIN	P30425 bothrops in
38	0	Nan	5	1 EI03_LITRU	P82099 litoria rub
39	0	Nan	5	1 EI04_LITRU	P82100 litoria rub
40	0	Nan	5	1 FARP_ARTTR	P41853 artiopesthi
41	0	Nan	5	1 FARP_CHICK	P83308 gallus gall
42	0	Nan	5	1 MPAJ4_JUNVI	P81826 juniperus v
43	0	Nan	5	1 PAP2_PARMA	P81864 pardachirus
44	0	Nan	5	1 PRCT_CARMA	P67857 carcinus ma
45	0	Nan	5	1 PRCT_LIMPO	P67858 limulus pol

ALIGNMENTS

RESULT 1
GWA_SEPOF STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis.";
RT Peptides 18:1469-1474(1997).
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity targeting the distal oviduct. Inhibits the motility of the oviduct by decreasing tonus, frequency and amplitude of contractions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 2 Tryptophan amide.
SQ SEQUENCE 2 AA; 261 MW; 737810000000000000 CRC64;

Query Match Nan%; Score 0; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 G 1

RESULT 2
GRWM_HUMAN STANDARD; PRT; 3 AA.
ID P01157;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL "Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC GO; GO:0001558; P:regulation of cell growth; NAS.
DR Direct protein sequencing.
KW SEQUENCE 3 AA; 340 MW; 6331E8100000000000 CRC64;
SQ

Query Match NaN; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 G 1

RESULT 3
LUXE_VIBFI
ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
DE Name=luxE;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
CC is a component of the fatty acid reductase complex responsible for
CC converting tetradecanoic acid to the aldehyde which serves as
CC substrate in the luciferase-catalyzed reaction.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thiolester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -!- SIMILARITY: Belongs to the luxE family.
CC -----
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CC -----
CC EMBL; M62812; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR Ligase; Luminescence.
KW NON TER 1
FT SEQUENCE 3 AA; 374 MW; 6AA330300000000000 CRC64;
SQ

Query Match NaN; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 I 1

RESULT 4
THYL_BOMOR
ID THYL_BOMOR STANDARD; PRT; 3 AA.
AC P62970; P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
DE releasing factor) (TSH-releasing factor) (Protirelin).
DE Bombina orientalis (Oriental fire-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8346;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
CC -!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
CC in the anterior pituitary gland and as a neurotransmitter/
CC neuromodulator in the central and peripheral nervous systems (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A90919; RHTDIO.
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 3 3 Proline amide.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B00000000000 CRC64;

Query Match NaN; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 5
THYL_NOTVI
ID THYL_NOTVI STANDARD; PRT; 3 AA.
AC P62971; P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
DE releasing factor) (TSH-releasing factor) (Protirelin).
DE Notoththalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notoththalmus.
OX NCBI_TaxID=8316;
RN [1]
RP PROTEIN SEQUENCE.


```
ACH1_ACHFU
ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Ferussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP CRYSTALLIZATION.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-
RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
RT residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
CC and produces a spike broadening of the identified heart excitatory
CC neuron (PON); also enhances the amplitude and frequency of the
CC heart beat. Has also an effect on several other muscles.
CC -----
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CC removed.
CC -----
DR PIR; A32480; A32480.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD_RES 2 D-phenylalanine.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match NaN; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1
Db 3 A 3

RESULT 9
DCML_PSECH
ID DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
dehydrogenase subunit L) (CO-DH L) (Fragment).

Query Match NaN; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1
Db 3 A 3

RESULT 10
DCMS_PSECH
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
DE Name=cutS;
GN Pseudomonas carboxydohydrogena.
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
CC -----
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GN Name=cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 1 Cu(+) ion per subunit.
CC -!- COFACTOR: Binds 1 Mo(6+) ion per subunit.
CC -!- COFACTOR: Binds 1 molybdopterin cytosine dinucleotide (MCD) per
CC subunit.
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
CC -----
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CC removed.
CC -----
DR PIR; PL0140; PL0140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON_TER 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match NaN; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1
Db 1 M 1

RESULT 10
DCMS_PSECH
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
DE Name=cutS;
GN Pseudomonas carboxydohydrogena.
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
CC -----
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CC -----
DR PIR; PL0146; PL0146.
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
KW Oxidoreductase.
FT NON TER 4 4
SQ - SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match      NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      2 A 2

RESULT 11
EOSI_HUMAN
ID EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eosinophilic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS: These peptides are released from mast cells in lung
CC (and other tissues) during hypersensitivity reactions
CC (anaphylaxis). Their activities, preferentially affecting
CC eosinophils, include chemotaxis, chemotactic deactivation, release
CC of enzymes, and stimulation of the hexose monophosphate shunt.
CC -----
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CC -----
CC GO; GO:0006935; P:chemotaxis; IDA.
CC GO; GO:0006955; P:immune response; IDA.
CC Direct protein sequencing.
CC VARIANT 1 1 V -> A (in other peptide).
CC SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match      NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      3 S 3

RESULT 12
FAR3_HIRME
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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removed.
-----
GO; GO:0006935; P:chemotaxis; IDA.
GO; GO:0006955; P:immune response; IDA.
Direct protein sequencing.
VARIANT 1 1 V -> A (in other peptide).
SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match      NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      3 S 3

RESULT 12
FAR3_HIRME
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
```

```
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide YLRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 4 4 phenylalanine amide.
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match      NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 Y 1

RESULT 13
FAR4_HIRME
ID FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 4 4 phenylalanine amide.
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match      NaN%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 Y 1
```

Db 1 Y 1

RESULT 14

FFKA ANTEL STANDARD; PRT; 4 AA.

AC P58705;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Antho-KAamide.

OS Anthopleura elegantissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthae; Actiniidae; Anthopleura.

OX NCBI_TaxID=6110;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=92028852; PubMed=1681803;

RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;

RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a

RT novel neuropeptide from sea anemones.";

RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two

RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle

CC groups. May be involved in the expansion phase of feeding

CC behaviour in sea anemones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Neuron specific.

CC

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CC

DR PIR; JQ1273; JQ1273.

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD_RES 1 1 3-phenyllactic acid.

FT MOD_RES 4 4 Alanine amide.

SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match NaN; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 4 A 4

RESULT 15

FLRF HELTI STANDARD; PRT; 4 AA.

AC P69138; P42561;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE FLRFamide.

OS Helisoma trivolvis (Snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;

OC Lymnaeidae; Planorbidae; Helisoma.

OX NCBI_TaxID=27815;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Kidney;

RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;

RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;

RT "FMRFamide-related peptides from the kidney of the snail, Helisoma

RT trivolvis.";

RL Peptides 15:31-36(1994).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)

CC family.

CC

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CC removed.

CC

KW Amidation; Direct protein sequencing; Neuropeptide.

FT MOD_RES 4 4 Phenylalanine amide.

SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match NaN; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 F 1

Search completed: May 2, 2006, 08:46:48

Job time : 92.6047 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 22.6977 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0
Sequence: 1 XXXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	Nan	1	1 US-07-820-154A-12	Sequence 12, Appl
2	0	Nan	1	1 US-07-791-213D-24	Sequence 24, Appl
3	0	Nan	1	1 US-07-791-213D-40	Sequence 40, Appl
4	0	Nan	1	1 US-08-174-365A-57	Sequence 57, Appl
5	0	Nan	1	1 US-07-789-913-23	Sequence 23, Appl
6	0	Nan	1	1 US-07-789-913-25	Sequence 25, Appl
7	0	Nan	1	1 US-08-049-794-23	Sequence 23, Appl
8	0	Nan	1	1 US-08-049-794-25	Sequence 25, Appl
9	0	Nan	1	1 US-08-433-037-12	Sequence 12, Appl
10	0	Nan	1	1 US-08-448-606-4	Sequence 4, Appl
11	0	Nan	1	1 US-07-869-933-16	Sequence 16, Appl
12	0	Nan	1	1 US-08-293-150A-24	Sequence 24, Appl
13	0	Nan	1	1 US-08-293-150A-40	Sequence 40, Appl
14	0	Nan	1	1 US-08-496-847-23	Sequence 23, Appl
15	0	Nan	1	1 US-08-496-847-25	Sequence 25, Appl
16	0	Nan	1	1 US-08-742-774-23	Sequence 23, Appl
17	0	Nan	1	1 US-08-742-774-25	Sequence 25, Appl
18	0	Nan	1	1 US-08-675-354-23	Sequence 23, Appl
19	0	Nan	1	1 US-08-675-354-25	Sequence 25, Appl
20	0	Nan	1	1 US-08-097-554A-12	Sequence 12, Appl
21	0	Nan	1	1 US-08-965-918-23	Sequence 23, Appl
22	0	Nan	1	1 US-08-965-918-25	Sequence 25, Appl
23	0	Nan	1	1 US-09-138-439-23	Sequence 23, Appl
24	0	Nan	1	1 US-09-138-439-25	Sequence 25, Appl
25	0	Nan	1	2 US-08-480-640A-12	Sequence 12, Appl
26	0	Nan	1	2 US-08-613-400A-23	Sequence 23, Appl
27	0	Nan	1	2 US-08-613-400A-25	Sequence 25, Appl

28	0	Nan	1	2 US-08-801-092-10	Sequence 10, Appl
29	0	Nan	1	2 US-08-801-092-17	Sequence 17, Appl
30	0	Nan	1	2 US-08-801-092-24	Sequence 24, Appl
31	0	Nan	1	2 US-08-801-092-31	Sequence 31, Appl
32	0	Nan	1	2 US-08-801-092-38	Sequence 38, Appl
33	0	Nan	1	2 US-08-801-092-45	Sequence 45, Appl
34	0	Nan	1	2 US-09-298-017-23	Sequence 23, Appl
35	0	Nan	1	2 US-09-298-017-25	Sequence 25, Appl
36	0	Nan	1	2 US-08-295-802-12	Sequence 12, Appl
37	0	Nan	1	2 US-09-392-979A-23	Sequence 23, Appl
38	0	Nan	1	2 US-09-392-979A-25	Sequence 25, Appl
39	0	Nan	1	2 US-09-103-663-16	Sequence 16, Appl
40	0	Nan	1	2 US-08-488-237A-12	Sequence 12, Appl
41	0	Nan	1	2 US-09-117-927-5	Sequence 5, Appl
42	0	Nan	1	2 US-08-375-992A-12	Sequence 12, Appl
43	0	Nan	1	2 US-09-315-113-10	Sequence 10, Appl
44	0	Nan	1	2 US-09-315-113-17	Sequence 17, Appl
45	0	Nan	1	2 US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-12
; Sequence 12, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,154A
; FILING DATE: 19920113
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-820-154A-12

Query Match Nan%; Score 0; DB 1; Length 1;
Best-Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 V 1

RESULT 2
US-07-791-213D-24

; Sequence 24, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-24

Query Match Nan%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 3
US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-40

Query Match Nan%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 4
US-08-174-365A-57
; Sequence 57, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seiichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified site
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
US-08-174-365A-57

Query Match
Best Local Similarity 100.0%; DB 1; Length 1;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 X 1

RESULT 5
US-07-789-913-23
Sequence 23, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23:
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO

Query Match
Best Local Similarity 100.0%; DB 1; Length 1;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 X 1

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-23
Query Match
Best Local Similarity 0.0%; DB 1; Length 1;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C.1

RESULT 6
US-07-789-913-25
Sequence 25, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-25

Query Match
Best Local Similarity 0.0%; DB 1; Length 1;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 7

US-08-049-794-23
; Sequence 23, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-049-794-23

Query Match

Best Local Similarity NaN%; Score 0; DB 1; Length 1;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 8

US-08-049-794-25
; Sequence 25, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-049-794-25

Query Match NaN%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 9

US-08-433-037-12
; Sequence 12, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
; APPLICANT: Brierley, Russell A.
; APPLICANT: Thill, Gregory P.
; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
; TITLE OF INVENTION: PICHIA PASTORIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9108Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-12

Query Match NaN% Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 L 1

RESULT 10
US-08-448-606-4
Sequence 4, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-606-4

Query Match NaN% Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Q 1

RESULT 11
US-07-869-933-16
Sequence 16, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-16

Query Match NaN% Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 M 1

RESULT 12
US-08-293-150A-24
Sequence 24, Application US/08293150A


```
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-24

Query Match      NaN;      Score 0;  DB 1;  Length 1;
Best Local Similarity 0.0%;  Pred. No. 0;
Matches 0;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1 X 1
Db      1 C 1

RESULT 13
US-08-293-150A-40
; Sequence 40, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
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```
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-40

Query Match      NaN;      Score 0;  DB 1;  Length 1;
Best Local Similarity 0.0%;  Pred. No. 0;
Matches 0;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1 X 1
Db      1 C 1

RESULT 14
US-08-496-847-23
; Sequence 23, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
```

; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
; US-08-496-847-23

Query Match Nan%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 C 1

RESULT 15
US-08-496-847-25
; Sequence 25, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: FORMULATIONS, FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
; US-08-496-847-25

Query Match Nan%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 R 1

Search completed: May 2, 2006, 08:58:26
Job time : 22.6977 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 74.4186 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 0

Sequence: 1 XXXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	NaN	1	3	US-09-778-885-5
2	0	NaN	1	3	US-09-909-348-4
3	0	NaN	1	3	US-09-982-172-3
4	0	NaN	1	3	US-09-982-172-4
5	0	NaN	1	3	US-09-982-172-9
6	0	NaN	1	3	US-09-982-172-11
7	0	NaN	1	3	US-09-982-172-19
8	0	NaN	1	3	US-09-982-172-31
9	0	NaN	1	3	US-09-982-172-35
10	0	NaN	1	3	US-09-982-172-37
11	0	NaN	1	3	US-09-982-172-46
12	0	NaN	1	3	US-09-982-172-69
13	0	NaN	1	3	US-09-982-172-80
14	0	NaN	1	3	US-09-982-172-81
15	0	NaN	1	3	US-09-982-172-83
16	0	NaN	1	3	US-09-982-172-86
17	0	NaN	1	3	US-09-982-172-93
18	0	NaN	1	3	US-09-982-172-95
19	0	NaN	1	3	US-09-982-172-106
20	0	NaN	1	3	US-09-982-172-112
21	0	NaN	1	3	US-09-982-172-120
22	0	NaN	1	3	US-09-982-172-126
23	0	NaN	1	3	US-09-982-172-148
24	0	NaN	1	3	US-09-982-172-149
25	0	NaN	1	3	US-09-982-172-155
26	0	NaN	1	3	US-09-982-172-160
27	0	NaN	1	3	US-09-982-172-172

28	0	NaN	1	3	US-09-982-172-173	Sequence 173, App
29	0	NaN	1	3	US-09-982-172-175	Sequence 175, App
30	0	NaN	1	3	US-09-982-172-189	Sequence 189, App
31	0	NaN	1	3	US-09-982-172-190	Sequence 190, App
32	0	NaN	1	3	US-09-982-172-191	Sequence 191, App
33	0	NaN	1	3	US-09-982-172-195	Sequence 195, App
34	0	NaN	1	3	US-09-982-172-200	Sequence 200, App
35	0	NaN	1	3	US-09-982-172-211	Sequence 211, App
36	0	NaN	1	3	US-09-809-391-395	Sequence 395, App
37	0	NaN	1	3	US-09-809-391-611	Sequence 611, App
38	0	NaN	1	3	US-09-882-171-395	Sequence 395, App
39	0	NaN	1	3	US-09-882-171-611	Sequence 611, App
40	0	NaN	1	3	US-09-833-245-184	Sequence 184, App
41	0	NaN	1	3	US-09-833-245-186	Sequence 186, App
42	0	NaN	1	3	US-09-833-245-325	Sequence 325, App
43	0	NaN	1	3	US-09-833-245-500	Sequence 500, App
44	0	NaN	1	3	US-09-833-245-744	Sequence 744, App
45	0	NaN	1	3	US-09-833-245-1045	Sequence 1045, Ap

ALIGNMENTS

RESULT 1
US-09-778-885-5
; Sequence 5, Application US/09778885
; Publication No. US20020039748A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR MAKING IT
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/778,885
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 60/087,032
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide motif
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
; OTHER INFORMATION: Pro, Trp or Val
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,
; OTHER INFORMATION: Tyr or Val
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,
; OTHER INFORMATION: Ser, Thr or Trp
; NAME/KEY: VARIANT
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
; OTHER INFORMATION: or Met
; NAME/KEY: VARIANT
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
; OTHER INFORMATION: Met, Phe or Trp
; NAME/KEY: VARIANT
; LOCATION: (8)...(8)

OTHER INFORMATION: Xaa is Gly or Glu
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr
NAME/KEY: VARIANT
LOCATION: (11)...(11)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Pro, Trp and Val
NAME/KEY: VARIANT
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: and Ser
NAME/KEY: VARIANT
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr
OTHER INFORMATION: or Trp
NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,
OTHER INFORMATION: Ser, Trp or Tyr
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,
OTHER INFORMATION: Met, Trp or Tyr
NAME/KEY: VARIANT
LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
NAME/KEY: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
NAME/KEY: VARIANT
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa is Tyr or Phe
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp
NAME/KEY: VARIANT
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
NAME/KEY: VARIANT
LOCATION: (22)...(22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
NAME/KEY: VARIANT
LOCATION: (23)...(23)
OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
NAME/KEY: VARIANT
LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
NAME/KEY: VARIANT
LOCATION: (25)...(25)
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 V 1

RESULT 2
US-09-909-348-4
; Sequence 4, Application US/09909348
; Patent No. US20020042373A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stienberg, Janet

APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin F
FILE REFERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION: (1)...(14)
OTHER INFORMATION: Xaa at position six is Glu or Gln
OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 V 1

RESULT 3
US-09-982-172-3
; Sequence 3, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENER
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 K 1

RESULT 4
US-09-982-172-4
; Sequence 4, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODI
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENER
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172

;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 5

US-09-982-172-9
; Sequence 9, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9.

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 6

US-09-982-172-11
; Sequence 11, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283.
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 7

US-09-982-172-19
; Sequence 19, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 8

US-09-982-172-31
; Sequence 31, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-31.

Query Match NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 9

US-09-982-172-35

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; Sequence 35, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-35

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 10
US-09-982-172-37
; Sequence 37, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-37

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 X 1
Db      1 K 1

RESULT 11
US-09-982-172-46
; Sequence 46, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-46

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 K 1

RESULT 12
US-09-982-172-69
; Sequence 69, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-69

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 K 1

RESULT 13
US-09-982-172-80
; Sequence 80, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-80

Query Match      NaN%; Score 0; DB 3; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 K 1
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Matches	0;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1 X 1								
Db	1 K 1								
RESULT 14									
US-09-982-172-81									
; Sequence 81, Application US/09982172									
; Patent No. US20020137119A1									
; GENERAL INFORMATION:									
; APPLICANT: Emil Israel Katz									
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES									
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING									
; TITLE OF INVENTION: UTILIZING EACH									
; FILE REFERENCE: 01/22283									
; CURRENT APPLICATION NUMBER: US/09/982,172									
; CURRENT FILING DATE: 2001-10-19									
; NUMBER OF SEQ ID NOS: 253									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 81									
; LENGTH: 1									
; TYPE: PRT									
; ORGANISM: Artificial sequence									
; FEATURE:									
; OTHER INFORMATION: Computer generated synthetic peptide									
US-09-982-172-81									
Query Match									
Best Local Similarity: 0.0%; Score 0; DB 3; Length 1;									
Pred. No. 0;									
Matches	0;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1 X 1								
Db	1 R 1								
RESULT 15									
US-09-982-172-83									
; Sequence 83, Application US/09982172									
; Patent No. US20020137119A1									
; GENERAL INFORMATION:									
; APPLICANT: Emil Israel Katz									
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES									
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING									
; TITLE OF INVENTION: UTILIZING EACH									
; FILE REFERENCE: 01/22283									
; CURRENT APPLICATION NUMBER: US/09/982,172									
; CURRENT FILING DATE: 2001-10-19									
; NUMBER OF SEQ ID NOS: 253									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 83									
; LENGTH: 1									
; TYPE: PRT									
; ORGANISM: Artificial sequence									
; FEATURE:									
; OTHER INFORMATION: Computer generated synthetic peptide									
US-09-982-172-83									
Query Match									
Best Local Similarity: 0.0%; Score 0; DB 3; Length 1;									
Pred. No. 0;									
Matches	0;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1 X 1								
Db	1 R 1								

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 11.3488 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-32
Perfect score: 0
Sequence: 1 XXXXXXXXX 8

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	NaN	1	11 US-11-078-256-279	Sequence 279, App
2	0	NaN	1	11 US-11-050-857-1142	Sequence 1142, Ap
3	0	NaN	1	11 US-11-144-947-395	Sequence 395, App
4	0	NaN	1	11 US-11-144-947-611	Sequence 611, App
5	0	NaN	1	11 US-11-264-096-184	Sequence 184, App
6	0	NaN	1	11 US-11-264-096-186	Sequence 186, App
7	0	NaN	1	11 US-11-264-096-325	Sequence 325, App
8	0	NaN	1	11 US-11-264-096-500	Sequence 500, App
9	0	NaN	1	11 US-11-264-096-744	Sequence 744, App
10	0	NaN	1	11 US-11-264-096-1045	Sequence 1045, Ap
11	0	NaN	1	11 US-11-264-096-1119	Sequence 1119, Ap
12	0	NaN	1	11 US-11-264-096-1546	Sequence 1546, Ap
13	0	NaN	2	9 US-10-877-961B-121	Sequence 121, App
14	0	NaN	2	9 US-10-913-711B-22	Sequence 22, Appl
15	0	NaN	2	9 US-10-509-095A-40	Sequence 40, Appl
16	0	NaN	2	9 US-10-509-095A-46	Sequence 46, Appl
17	0	NaN	2	9 US-10-971-359A-2	Sequence 2, Appli
18	0	NaN	2	9 US-10-971-359A-3	Sequence 3, Appli
19	0	NaN	2	9 US-10-496-845A-7	Sequence 7, Appli
20	0	NaN	2	9 US-10-760-085-42	Sequence 42, Appl
21	0	NaN	2	9 US-10-644-807-322	Sequence 322, App

22	0	NaN	2	11 US-11-043-806-531	Sequence 531, Appl
23	0	NaN	2	11 US-11-149-015-9	Sequence 9, Appli
24	0	NaN	2	11 US-11-149-015-54	Sequence 54, Appl
25	0	NaN	2	11 US-11-148-262-1	Sequence 1, Appli
26	0	NaN	2	11 US-11-148-262-2	Sequence 2, Appli
27	0	NaN	2	11 US-11-148-262-3	Sequence 3, Appli
28	0	NaN	2	11 US-11-148-262-4	Sequence 4, Appli
29	0	NaN	2	11 US-11-148-262-5	Sequence 5, Appli
30	0	NaN	2	11 US-11-148-262-6	Sequence 6, Appli
31	0	NaN	2	11 US-11-148-262-8	Sequence 8, Appli
32	0	NaN	2	11 US-11-148-262-9	Sequence 9, Appli
33	0	NaN	2	11 US-11-148-262-10	Sequence 10, Appl
34	0	NaN	2	11 US-11-148-262-11	Sequence 11, Appl
35	0	NaN	2	11 US-11-148-262-12	Sequence 12, Appl
36	0	NaN	2	11 US-11-148-262-13	Sequence 13, Appl
37	0	NaN	2	11 US-11-148-266-1	Sequence 1, Appli
38	0	NaN	2	11 US-11-148-266-2	Sequence 2, Appli
39	0	NaN	2	11 US-11-148-266-3	Sequence 3, Appli
40	0	NaN	2	11 US-11-148-266-4	Sequence 4, Appli
41	0	NaN	2	11 US-11-148-266-5	Sequence 5, Appli
42	0	NaN	2	11 US-11-148-266-6	Sequence 6, Appli
43	0	NaN	2	11 US-11-148-266-8	Sequence 8, Appli
44	0	NaN	2	11 US-11-148-266-9	Sequence 9, Appli
45	0	NaN	2	11 US-11-148-266-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-11-078-256-279
; Sequence 279, Application US/11078256
; Publication No. US20060035814A1
; GENERAL INFORMATION:
; APPLICANT: Brophy, Colleen
; APPLICANT: Komalavilas, Padmini
; APPLICANT: Panitch, Alyssa
; APPLICANT: Joshi, Lokesh
; APPLICANT: Seal, Brandon L.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
; FILE REFERENCE: 03-223-US
; CURRENT APPLICATION NUMBER: US/11/078,256
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/314,535
; PRIOR FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 279
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is (R)4-9
US-11-078-256-279

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 X 1
|
Db 1 X 1

RESULT 2
US-11-050-857-1142
; Sequence 1142, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:

; APPLICANT: CompuGen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 1142
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-050-857-1142

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 E 1

RESULT 3
US-11-144-947-395
; Sequence 395, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 395
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-947-395

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 M 1

RESULT 4

US-11-144-947-611
; Sequence 611, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 611
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-947-611

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 M 1

RESULT 5
US-11-264-096-184
; Sequence 184, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF545D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-184

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 S 1

RESULT 6

US-11-264-096-186
; Sequence 186, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-186

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 S 1

RESULT 7

US-11-264-096-325
; Sequence 325, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 325
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-325

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 I 1

RESULT 8

US-11-264-096-500
; Sequence 500, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-500

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 M 1

RESULT 9

US-11-264-096-744
; Sequence 744, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 744
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-744

Query Match Nan%; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 N 1

RESULT 10

US-11-264-096-1045
; Sequence 1045, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1045
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1045

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 11

US-11-264-096-1119
; Sequence 1119, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1119
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1119

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 X 1

Db 1 A 1

RESULT 12

US-11-264-096-1546
; Sequence 1546, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1546
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1546

Query Match NaN; Score 0; DB 11; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 M 1

RESULT 13

US-10-877-961B-121
; Sequence 121, Application US/10877961B
; Publication No. US20060003941A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: Kawabe, Takumi
; APPLICANT: Kobayashi, Hidetaka
; TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS HAVING IMMUNE-MODULATING, ANTI-
; TITLE OF INVENTION: INFLAMMATORY, AND ANTI-VIRAL ACTIVITY
; FILE REFERENCE: 087533-0309084
; CURRENT APPLICATION NUMBER: US/10/877,961B
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: PCT/IB2004/002591
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: 60/482,750
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Positions 1 to 2 are D-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa is D-Phenylalanine-2,3,4,5,6-F
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa is D-Cyclohexyl-alanine
US-10-877-961B-121

Query Match Nan%; Score 0; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1
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Db 1 X 1

RESULT 14
US-10-913-711B-22
; Sequence 22, Application US/10913711B
; Publication No. US20060014157A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: Kawabe, Takumi
; APPLICANT: Kobayashi, Hidetaka
; TITLE OF INVENTION: SENSITIVITY TEST TO PREDICT EFFICACY OF ANTI-CANCER THERAPIES
; FILE REFERENCE: 087533-0310448
; CURRENT APPLICATION NUMBER: US/10/913,711B
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: 60/494,022
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Positions 1 to 2 are D-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is D-Phenylalanine-2,3,4,5,6-F
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa is D-Cyclohexyl-alanine
US-10-913-711B-22

Query Match Nan%; Score 0; DB 9; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1
 |
Db 1 X 1

RESULT 15
US-10-509-095A-40
; Sequence 40, Application US/10509095A
; Publication No. US20060036073A1
; GENERAL INFORMATION:
; APPLICANT: WINDISCH, MANFRED
; TITLE OF INVENTION: NEUTROPHIC AND NEUROPROTECTIVE PEPTIDES
; FILE REFERENCE: 4301-1117
; CURRENT APPLICATION NUMBER: US/10/509,095A
; CURRENT FILING DATE: 2004-09-28
; PRIOR APPLICATION NUMBER: PCT/AT03/00065
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: AT A 495/2002
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 40
; LENGTH: 2

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-509-095A-40

Query Match Nan%; Score 0; DB 9; Length 2;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
 |
Db 1 G 1

Search completed: May 2, 2006, 09:33:44
Job time : 11.3488 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 28.3721 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	14	1	US-08-727-688-23
2	18	100.0	167	2	US-09-252-991A-17897
3	18	100.0	191	2	US-09-252-991A-25365
4	18	100.0	438	2	US-09-252-991A-31307
5	18	100.0	777	2	US-09-270-767-44409
6	18	100.0	801	1	US-07-906-349A-6
7	18	100.0	1152	2	US-09-303-518D-195
8	18	100.0	1388	2	US-09-463-048A-6
9	18	100.0	1497	2	US-09-060-854B-2
10	18	100.0	1497	2	US-09-529-904-3
11	18	100.0	1917	2	US-09-627-650B-5
12	18	100.0	1917	2	US-09-436-063C-5
13	18	100.0	2616	2	US-09-303-518D-879
14	17	94.4	45	1	US-08-824-379-3
15	17	94.4	48	4	PCT-US96-01720-9
16	17	94.4	150	2	US-09-252-991A-31728
17	17	94.4	156	2	US-09-252-991A-20612
18	17	94.4	169	2	US-09-252-991A-20344
19	17	94.4	169	2	US-09-252-991A-24301
20	17	94.4	172	2	US-09-252-991A-23050
21	17	94.4	180	2	US-09-303-518D-603
22	17	94.4	191	2	US-09-252-991A-19331
23	17	94.4	200	2	US-09-252-991A-22497
24	17	94.4	204	2	US-09-252-991A-31049
25	17	94.4	222	2	US-09-252-991A-26487
26	17	94.4	229	2	US-09-252-991A-29247
27	17	94.4	243	2	US-09-252-991A-25814

28	17	94.4	281	2	US-09-252-991A-29199	Sequence 29199, A
29	17	94.4	314	2	US-09-252-991A-31368	Sequence 31368, A
30	17	94.4	341	1	US-08-209-521-11	Sequence 11, Appl
31	17	94.4	414	2	US-09-252-991A-25096	Sequence 25096, A
32	17	94.4	684	2	US-09-303-518D-721	Sequence 721, Appl
33	17	94.4	908	2	US-08-714-741-44	Sequence 44, Appl
34	17	94.4	1400	2	US-08-630-915A-37	Sequence 37, Appl
35	17	94.4	1400	2	US-09-879-957-37	Sequence 37, Appl
36	17	94.4	1461	2	US-10-142-231-86	Sequence 86, Appl
37	17	94.4	1652	2	US-09-627-650B-1	Sequence 1, Appl
38	17	94.4	1652	2	US-09-436-063C-1	Sequence 1, Appl
39	17	94.4	2508	2	US-09-627-650B-7	Sequence 7, Appl
40	17	94.4	2508	2	US-09-436-063C-7	Sequence 7, Appl
41	17	94.4	2544	2	US-09-627-650B-3	Sequence 3, Appl
42	17	94.4	2544	2	US-09-436-063C-3	Sequence 3, Appl
43	17	94.4	2601	2	US-09-627-650B-9	Sequence 9, Appl
44	17	94.4	2601	2	US-09-436-063C-9	Sequence 9, Appl
45	17	94.4	2732	2	US-09-086-436-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-08-727-688-23
; Sequence 23, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foremski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
US-08-727-688-23

Query Match 100.0%; Score 18; DB 1; Length 14;
Best Local Similarity 20.0%; Pred. No. 0.21;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CXXXXXXXC 10

Db 3 C555555SAC 12

RESULT 2

US-09-252-991A-17897

; Sequence 17897, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17897

; LENGTH: 167

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17897

Query Match 100.0%; Score 18; DB 2; Length 167;

Best Local Similarity 20.0%; Pred. No. 0.35;

Matches 2; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

Qy 1 CXXXXXXXC 10

Db 60 CSTSTSTSC 69

RESULT 3

US-09-252-991A-25365

; Sequence 25365, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25365

; LENGTH: 191

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25365

Query Match 100.0%; Score 18; DB 2; Length 191;

Best Local Similarity 20.0%; Pred. No. 0.36;

Matches 2; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

Qy 1 CXXXXXXXC 10

Db 49 CSTAASATSC 58

RESULT 4

US-09-252-991A-31307

; Sequence 31307, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 31307

; LENGTH: 438

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31307

Query Match 100.0%; Score 18; DB 2; Length 438;

Best Local Similarity 20.0%; Pred. No. 0.43;

Matches 2; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

Qy 1 CXXXXXXXC 10

Db 56 CSAATASSTC 65

RESULT 5

US-09-270-767-44409

; Sequence 44409, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 44409

; LENGTH: 777

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-44409

Query Match 100.0%; Score 18; DB 2; Length 777;

Best Local Similarity 20.0%; Pred. No. 0.48;

Matches 2; Conservative 0; Mismatches 8; Indels 8; Gaps 0;

Qy 1 CXXXXXXXC 10

Db 729 CSTSSSSSSC 738

RESULT 6

US-07-906-349A-6

; Sequence 6, Application US/07906349A

; Patent No. 5434064

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnik, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES

; TITLE OF INVENTION: TARGET PROTEINS

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,349A
; FILING DATE: 30-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/643,237
; FILING DATE: 18-JAN-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 801 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-906-349A-6

Query Match 100.0%; Score 18; DB 1; Length 801;
Best Local Similarity 20.0%; Pred. No. 0.48;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 608 CTTTTTTTC 617

RESULT 7

US-09-303-518D-195
; Sequence 195, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-09-303-518D-195

Query Match 100.0%; Score 18; DB 2; Length 1152;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 1138 CAAAAAATAC 1147

RESULT 8

US-09-463-048A-6
; Sequence 6, Application US/09463048A
; Patent No. 6630619
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photox
; TITLE OF INVENTION: luminescens
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/09/463,048A

; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
; US-09-463-048A-6

Query Match 100.0%; Score 18; DB 2; Length 1388;
Best Local Similarity 20.0%; Pred. No. 0.53;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 8 CTAATAATTC 17

RESULT 9

US-09-060-854B-2
; Sequence 2, Application US/09060854B
; Patent No. 6642011
; GENERAL INFORMATION:
; APPLICANT: Estell, David Aaron
; TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
; TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: GC532
; CURRENT APPLICATION NUMBER: US/09/060,854B
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
; US-09-060-854B-2

Query Match 100.0%; Score 18; DB 2; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.54;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 30 CAATTAATAC 39

RESULT 10

US-09-529-904-3
; Sequence 3, Application US/09529904
; Patent No. 6831053
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Chanchal K.
; APPLICANT: Baeck, Andre C.
; APPLICANT: Ohtani, Ryohei (nmn)
; APPLICANT: Busch, Alfred (nmn)
; APPLICANT: Showell, Michael S.
; APPLICANT: Poulse, Ayrookaran J.
; APPLICANT: Schellenberger, Volker (nmn)
; APPLICANT: Kellis, Jr., James T.
; APPLICANT: Paech, Christian (nmn)
; APPLICANT: Nadherny, Joanne (nmn)
; APPLICANT: Naki, Donald P.
; APPLICANT: Collier, Katherine D.
; APPLICANT: Caldwell, Robert M.
; TITLE OF INVENTION: Bleaching compositions comprising multiply-substituted
; TITLE OF INVENTION: protease variants
; FILE REFERENCE: Bleaching comp comprising multiply-sub
; CURRENT APPLICATION NUMBER: US/09/529,904

```
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 08/956,323
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: US 08/956,564
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: US 08/956,324
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-529-904-3

Query Match      100.0%; Score 18; DB 2; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.54;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXXC 10
Db      30 CAATTAATAC 39

RESULT 11
US-09-627-650B-5
; Sequence 5, Application US/09627650B
; Patent No. 6406872
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 21101.0009U3
; CURRENT APPLICATION NUMBER: US/09/627,650B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107,727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-627-650B-5

Query Match      100.0%; Score 18; DB 2; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.57;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXXC 10
Db      1049 CAAATATATC 1058

RESULT 12
US-09-436-063C-5
; Sequence 5, Application US/09436063C
; Patent No. 6407210
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: P-1095corrected
; CURRENT APPLICATION NUMBER: US/09/436,063C
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-436-063C-5

Query Match      100.0%; Score 18; DB 2; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.57;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXXC 10
Db      1049 CAAATATATC 1058

US-09-436-063C-5
; Sequence 5, Application US/0930303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 879
; LENGTH: 2616
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-879

Query Match      100.0%; Score 18; DB 2; Length 2616;
Best Local Similarity 20.0%; Pred. No. 0.61;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXXC 10
Db      876 CAATAAATAC 885

RESULT 14
US-08-824-379-3
; Sequence 3, Application US/08824379
; Patent No. 5885801
; GENERAL INFORMATION:
; APPLICANT: Rao, A. Gururaj
; TITLE OF INVENTION: High Threonine Derivatives of
; TITLE OF INVENTION: Alpha-Hordothionin
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States of America
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/459,180
```


ATTORNEY/AGENT INFORMATION:
NAME: Simon, Soma G.
REGISTRATION NUMBER: 37,444
REFERENCE/DOCKET NUMBER: 354-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-248-4896
TELEFAX: 515-248-4844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-824-379-3

Query Match 94.4%; Score 17; DB 1; Length 45;
Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
Db 16 CTTTATTTC 25

RESULT 15
PCT-US96-01720-9
Sequence 9, Application PC/TUS9601720
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01720
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,055
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 16336-5PC
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-01720-9

Query Match 94.4%; Score 17; DB 4; Length 48;
Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
Db 3 CGTTTAAATC 12

Search completed: May 2, 2006, 08:58:25
Job time : 28.3721 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 112.791 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	30	9 ADZ47471	Adz47471 Alu sense
2	18	100.0	89	8 ADP30533	Adp30533 Human sec
3	18	100.0	89	8 ADP30531	Adp30531 Human sec
4	18	100.0	109	4 AAM93527	Aam93527 Human pol
5	18	100.0	109	8 ADL31230	Adl31230 Human pro
6	18	100.0	109	8 ADP30690	Adp30690 Human sec
7	18	100.0	144	8 ADP31474	Adp31474 Human sec
8	18	100.0	167	7 ABO69151	Abo69151 Pseudomon
9	18	100.0	169	8 ADS12185	Adsl2185 Human the
10	18	100.0	171	8 ADP30794	Adp30794 Human sec
11	18	100.0	171	8 ADP30793	Adp30793 Human sec
12	18	100.0	183	8 ADP30806	Adp30806 Human sec
13	18	100.0	191	7 ABO76619	Abo76619 Pseudomon
14	18	100.0	214	9 ADZ56213	Adz56213 Human KIA
15	18	100.0	228	8 ADP30921	Adp30921 Human sec
16	18	100.0	252	8 ADP31485	Adp31485 Human sec
17	18	100.0	258	8 ADP30479	Adp30479 Human sec
18	18	100.0	264	8 ADP31412	Adp31412 Human sec
19	18	100.0	270	8 ADP30500	Adp30500 Human sec
20	18	100.0	270	8 ADP31321	Adp31321 Human sec
21	18	100.0	294	8 ADP31473	Adp31473 Human sec
22	18	100.0	297	8 ADP31192	Adp31192 Human sec
23	18	100.0	328	4 AAM25285	Aam25285 Human pro
24	18	100.0	339	8 ADP30702	Adp30702 Human sec

25	18	100.0	348	8 ADP31441	Adp31441 Human sec
26	18	100.0	356	4 ABG21039	Abg21039 Novel hum
27	18	100.0	357	8 ADP31267	Adp31267 Human sec
28	18	100.0	357	8 ADP30505	Adp30505 Human sec
29	18	100.0	360	8 ADP31439	Adp31439 Human sec
30	18	100.0	390	8 ADP31218	Adp31218 Human sec
31	18	100.0	421	8 ADP31159	Adp31159 Human sec
32	18	100.0	426	8 ADP31495	Adp31495 Human sec
33	18	100.0	438	7 ABO82561	Abo82561 Pseudomon
34	18	100.0	453	8 ADP31465	Adp31465 Human sec
35	18	100.0	471	8 ADP30854	Adp30854 Human sec
36	18	100.0	525	8 ADP31227	Adp31227 Human sec
37	18	100.0	549	8 ADP30855	Adp30855 Human sec
38	18	100.0	555	8 ADP31416	Adp31416 Human sec
39	18	100.0	555	8 ADP31417	Adp31417 Human sec
40	18	100.0	588	8 ADP31699	Adp31699 Human sec
41	18	100.0	591	9 ADZ56209	Adz56209 Human KIA
42	18	100.0	591	9 ADZ56223	Adz56223 Human KIA
43	18	100.0	600	8 ADP30865	Adp30865 Human sec
44	18	100.0	604	8 ADP30940	Adp30940 Human sec
45	18	100.0	604	8 ADP30941	Adp30941 Human sec

ALIGNMENTS

RESULT 1
ADZ47471
ID ADZ47471 standard; peptide; 30 AA.

XX ADZ47471;
XX
DT 30-JUN-2005 (first entry)
XX
DE Alu sense peptide SEQ ID NO 50.

XX hyaluronan synthase; HAS; hyaluronidase; HYAL; HAS1; HAS2; HAS3; HYAL1;
KW HYAL2; HAL3; PH-20; cancer; hyperproliferation; inflammation; anabolic;
KW hypertensive; gynaecological; neuroprotective; antianemic; cytostatic;
KW anti-inflammatory; endocrine-gen; immunosuppressive; gene therapy.

XX Unidentified.
OS
XX
PN WO2005035548-A1.

XX
PD 21-APR-2005.

XX
PF 11-OCT-2004; 2004WO-AU001383.

XX
PR 10-OCT-2003; 2003AU-00905551.

XX
PR 01-DEC-2003; 2003AU-00906658.

XX (MEDI-) MEDITECH RES LTD.

XX Brown TJ, Brownlee GR;

XX WPI; 2005-315540/32.

XX Novel compound capable of reducing level, function or activity of
PT hyaluronan synthase or hyaluronidase, useful for treating cancer,
PT hyperproliferative condition, A-beta-lipoproteinemia, A-V, A beta-2-
PT microglobulin amyloidosis.

XX Example 22; SEQ ID NO 50; 277pp; English.

XX This invention describes a novel nucleic acid molecule capable of
CC reducing the level of hyaluronan synthase (HAS) or hyaluronidase (HYAL)
CC or the function or activity of HAS or HYAL. HAS is selected from HAS1,
CC HAS2 and HAS3. HYAL is chosen from HYAL1, HYAL2, HAL3 and PH-20. The
CC nucleic acid molecule is an oligonucleotide or its chemically modified
CC form comprising a chemically modified backbone or a non-natural
CC internucleoside linkage. The compound is an interactive molecule capable
CC of binding or otherwise associating with HAS and/or HYAL to reduce HAS

CC and/or HYAL function or activity. The novel molecule is useful for
CC treating cancer, hyperproliferative conditions or inflammatory
CC conditions. The products of the invention are useful for treating or
CC prophylaxis of a condition in subject, which involves administering to
CC the subject, an HAS and/or HYAL level-reducing or HAS and/or HYAL
CC activity reducing effective amount of active molecule. The products of
CC the invention have anabolic, hypertensive, gynaecological,
CC neuroprotective, antianemic, cytostatic, anti-inflammatory, endocrine-
CC gen. and immunosuppressive activity. This sequence represents a peptide
CC used in the method of the invention. NOTE: The specification describes
CC SEQ ID NO 27-51 as nucleotide primers however the Sequence Listing
CC represents the nucleotides in a three letter amino acid code. The
CC nucleotide sequences have been made and are represented in { }.

XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 18; DB 9; Length 30;
Best Local Similarity 20.0%; Pred. No. 2.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
Db 18 CTAATAATAC 27

RESULT 2
ADP30533
ID ADP30533 standard; protein; 89 AA.

XX ADP30533;

DT 12-AUG-2004 (first entry)

DE Human secreted protein SEQ ID #1300.

XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.

XX Homo sapiens.

PN WO2004035732-A2.

XX 29-APR-2004.

PF 28-AUG-2003; 2003WO-US026780.

XX 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.

PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2531; 428pp; English.

The present invention relates to an isolated nucleic acid molecule
encoding a polypeptide which is believed to be cytostatic,
antiinflammatory, immunosuppressive, antibacterial and virucidal. The
composition and methods are useful for diagnosing, preventing and
treating diseases such as proliferative (e.g. cancer), inflammatory,
immune, metabolic, genetic, bacterial and viral diseases. The present
sequence represents a human secreted protein. The present sequence is
available on WIPOWEB and is not in the specification.

Sequence 89 AA;

Query Match 100.0%; Score 18; DB 8; Length 89;
Best Local Similarity 20.0%; Pred. No. 3.1;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|

Db 24 CTTAAAAAAC 33

RESULT 3

ADP30531

ID ADP30531 standard; protein; 89 AA.

XX

AC ADP30531;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human secreted protein SEQ ID #1298.

XX

KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;

KW cancer; inflammatory; immune; human secreted protein.

XX

OS Homo sapiens.

XX

PN WO2004035732-A2.

XX

PD 29-APR-2004.

XX

PF 28-AUG-2003; 2003WO-US026780.

XX

PR 29-AUG-2002; 2002US-0406576P.

PR 29-AUG-2002; 2002US-0406579P.

PR 29-AUG-2002; 2002US-0406585P.

PR 29-AUG-2002; 2002US-0406588P.

PR 29-AUG-2002; 2002US-0406588P.

PR 29-AUG-2002; 2002US-0406608P.

PR 29-AUG-2002; 2002US-0406611P.

PR 29-AUG-2002; 2002US-0406612P.

PR 29-AUG-2002; 2002US-0406616P.

PR 29-AUG-2002; 2002US-0406640P.

PR 29-AUG-2002; 2002US-0406642P.

PR 29-AUG-2002; 2002US-0406646P.

PR 29-AUG-2002; 2002US-0406653P.

PR 29-AUG-2002; 2002US-0406655P.

PR 29-AUG-2002; 2002US-0406666P.

PR 17-SEP-2002; 2002US-0410946P.

PR 17-SEP-2002; 2002US-0410947P.

PR 17-SEP-2002; 2002US-0410948P.

PR 17-SEP-2002; 2002US-0410949P.

PR 17-SEP-2002; 2002US-0410953P.

PR 17-SEP-2002; 2002US-0410957P.

PR 17-SEP-2002; 2002US-0410958P.

PR 17-SEP-2002; 2002US-0410959P.

PR 17-SEP-2002; 2002US-0410960P.

PR 17-SEP-2002; 2002US-0410961P.

PR 17-SEP-2002; 2002US-0410962P.

PR 17-SEP-2002; 2002US-0411019P.

PR 17-SEP-2002; 2002US-0411022P.

PR 17-SEP-2002; 2002US-0411023P.

PR 17-SEP-2002; 2002US-0411024P.

PR 17-SEP-2002; 2002US-0411032P.

PR 17-SEP-2002; 2002US-0411035P.

PR 17-SEP-2002; 2002US-0411037P.

PR 17-SEP-2002; 2002US-0411041P.

PR 17-SEP-2002; 2002US-0411045P.

PR 17-SEP-2002; 2002US-0411046P.

PR 17-SEP-2002; 2002US-0411048P.

PR 17-SEP-2002; 2002US-0411052P.

PR 17-SEP-2002; 2002US-0411055P.

PR 17-SEP-2002; 2002US-0411055P.

PR 17-SEP-2002; 2002US-0411073P.

PR 17-SEP-2002; 2002US-0411082P.

PR 17-SEP-2002; 2002US-0411101P.

PR 17-SEP-2002; 2002US-0411111P.

PR 18-APR-2003; 2003US-0463700P.

PR 18-APR-2003; 2003US-0463708P.

PR 18-APR-2003; 2003US-0463716P.

PR 18-APR-2003; 2003US-0463732P.

PR 02-MAY-2003; 2003US-0467199P.

PR 02-MAY-2003; 2003US-0467201P.

PR 02-MAY-2003; 2003US-0467203P.

PR

02-MAY-2003; 2003US-0467230P.

PR 19-MAY-2003; 2003US-0471306P.

PR 19-MAY-2003; 2003US-0471336P.

PR 22-MAY-2003; 2003US-0472420P.

PR 22-MAY-2003; 2003US-0472430P.

PR 09-JUN-2003; 2003US-0476609P.

PR 09-JUN-2003; 2003US-0476641P.

PR 08-JUL-2003; 2003US-0485218P.

PR 08-JUL-2003; 2003US-0485223P.

PR 08-JUL-2003; 2003US-0485224P.

PR 08-JUL-2003; 2003US-0485325P.

PR 14-JUL-2003; 2003US-0486446P.

PR 14-JUL-2003; 2003US-0486480P.

PR 15-JUL-2003; 2003US-0486891P.

PR 15-JUL-2003; 2003US-0486960P.

PR 08-AUG-2003; 2003US-0493341P.

PR 08-AUG-2003; 2003US-0493370P.

PR 08-AUG-2003; 2003US-0493573P.

PR 08-AUG-2003; 2003US-0493577P.

XX

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX

PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;

PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;

PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

XX

DR WPI; 2004-348438/32.

XX

PT New nucleic acid molecule for diagnosing, preventing or treating diseases

PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,

PT genetic, bacterial and viral diseases.

XX

PS Claim 1; SEQ ID NO 2529; 428pp; English.

XX

CC The present invention relates to an isolated nucleic acid molecule

CC encoding a polypeptide which is believed to be cytostatic,

CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The

CC composition and methods are useful for diagnosing, preventing and

CC treating diseases such as proliferative (e.g. cancer), inflammatory,

CC immune, metabolic, genetic, bacterial and viral diseases. The present

CC sequence represents a human secreted protein. The present sequence is

CC available on WIPOWEB and is not in the specification.

XX

SQ Sequence 89 AA;

Query Match 100.0%; Score 18; DB 8; Length 89;

Best local Similarity 20.0%; Pred. No. 3.1;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 24 CTTAAAAAAC 33

RESULT 4

AAM93527

ID AAM93527 standard; protein; 109 AA.

XX

AC AAM93527;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3263.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.


```
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
PA
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94457.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3263; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 109 AA;
Query Match 100.0%; Score 18; DB 4; Length 109;
Best Local Similarity 20.0%; Pred. No. 3.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1 CXXXXXXXXC 10
Db 4 CSSSATSTSC 13
RESULT 5
ADL31230
ID ADL31230 standard; protein; 109 AA.
XX
AC ADL31230;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein encoded by a full length cDNA clone SeqID 3263.
XX
KW human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
XX WPI; 2004-204755/20.
DR N-PSDB; ADL31229.
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX
XX Example 1; SEQ ID NO 3263; 1340pp; English.
XX
CC This invention relates to a novel primers useful for synthesising full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
CC length human protein of the invention.
XX
SQ Sequence 109 AA;
Query Match 100.0%; Score 18; DB 8; Length 109;
Best Local Similarity 20.0%; Pred. No. 3.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1 CXXXXXXXXC 10
Db 4 CSSSATSTSC 13
RESULT 6
ADP30690
ID ADP30690 standard; protein; 109 AA.
XX
AC ADP30690;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human secreted protein SEQ ID #1457.
XX
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
PN WO2004035732-A2.
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
```

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1 CXXXXXXXC 10
Db	96 CTTTATATC 105
RESULT 7	
ADP31474	
ID	ADP31474 standard; protein; 144 AA.
XX	
AC	ADP31474;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Human secreted protein SEQ ID #2241.
XX	
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW	cancer; inflammatory; immune; human secreted protein.
XX	
OS	Homo sapiens.
XX	
PN	WO2004035732-A2.
XX	
PD	29-APR-2004.
XX	
PF	28-AUG-2003; 2003WO-US026780.
XX	
PR	29-AUG-2002; 2002US-0406576P.
PR	29-AUG-2002; 2002US-0406579P.
PR	29-AUG-2002; 2002US-0406585P.
PR	29-AUG-2002; 2002US-0406588P.
PR	29-AUG-2002; 2002US-0406608P.
PR	29-AUG-2002; 2002US-0406611P.
PR	29-AUG-2002; 2002US-0406612P.
PR	29-AUG-2002; 2002US-0406616P.
PR	29-AUG-2002; 2002US-0406640P.
PR	29-AUG-2002; 2002US-0406642P.
PR	29-AUG-2002; 2002US-0406646P.
PR	29-AUG-2002; 2002US-0406653P.
PR	29-AUG-2002; 2002US-0406655P.
PR	29-AUG-2002; 2002US-0406666P.
PR	17-SEP-2002; 2002US-0410946P.
PR	17-SEP-2002; 2002US-0410947P.
PR	17-SEP-2002; 2002US-0410948P.
PR	17-SEP-2002; 2002US-0410949P.
PR	17-SEP-2002; 2002US-0410953P.
PR	17-SEP-2002; 2002US-0410957P.
PR	17-SEP-2002; 2002US-0410958P.
PR	17-SEP-2002; 2002US-0410959P.
PR	17-SEP-2002; 2002US-0410960P.
PR	17-SEP-2002; 2002US-0410961P.
PR	17-SEP-2002; 2002US-0410962P.
PR	17-SEP-2002; 2002US-0411019P.
PR	17-SEP-2002; 2002US-0411022P.
PR	17-SEP-2002; 2002US-0411023P.
PR	17-SEP-2002; 2002US-0411024P.
PR	17-SEP-2002; 2002US-0411032P.
PR	17-SEP-2002; 2002US-0411035P.
PR	17-SEP-2002; 2002US-0411037P.
PR	17-SEP-2002; 2002US-0411041P.
PR	17-SEP-2002; 2002US-0411045P.
PR	17-SEP-2002; 2002US-0411046P.
PR	17-SEP-2002; 2002US-0411048P.
PR	17-SEP-2002; 2002US-0411052P.
PR	17-SEP-2002; 2002US-0411055P.
PR	17-SEP-2002; 2002US-0411073P.
PR	17-SEP-2002; 2002US-0411082P.
PR	17-SEP-2002; 2002US-0411082P.
PR	17-SEP-2002; 2002US-0411101P.
PR	17-SEP-2002; 2002US-0411111P.
PR	18-APR-2003; 2003US-0463700P.
PR	18-APR-2003; 2003US-0463708P.
PR	18-APR-2003; 2003US-0463716P.

PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases
such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2688; 428pp; English.

The present invention relates to an isolated nucleic acid molecule
encoding a polypeptide which is believed to be cytostatic,
antiinflammatory, immunosuppressive, antibacterial and virucidal. The
composition and methods are useful for diagnosing, preventing and
treating diseases such as proliferative (e.g. cancer), inflammatory,
immune, metabolic, genetic, bacterial and viral diseases. The present
sequence represents a human secreted protein. The present sequence is
available on WIPWEB and is not in the specification.

XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 18; DB 8; Length 109;
Best Local Similarity 20.0%; Pred. No. 3.2;

PR18-APR-2003; 2003US-0463732P.
PR02-MAY-2003; 2003US-0467199P.
PR02-MAY-2003; 2003US-0467201P.
PR02-MAY-2003; 2003US-0467203P.
PR02-MAY-2003; 2003US-0467230P.
PR19-MAY-2003; 2003US-0471306P.
PR19-MAY-2003; 2003US-0471336P.
PR22-MAY-2003; 2003US-0472420P.
PR22-MAY-2003; 2003US-0472430P.
PR09-JUN-2003; 2003US-0476609P.
PR08-JUL-2003; 2003US-0476641P.
PR08-JUL-2003; 2003US-0485218P.
PR08-JUL-2003; 2003US-0485223P.
PR08-JUL-2003; 2003US-0485224P.
PR08-JUL-2003; 2003US-0485325P.
PR14-JUL-2003; 2003US-0486446P.
PR14-JUL-2003; 2003US-0486480P.
PR15-JUL-2003; 2003US-0486891P.
PR15-JUL-2003; 2003US-0486960P.
PR08-AUG-2003; 2003US-0493341P.
PR08-AUG-2003; 2003US-0493370P.
PR08-AUG-2003; 2003US-0493573P.
PR08-AUG-2003; 2003US-0493577P.
XX
PA(FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PIWilliams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PIHalenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PIPierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DRWPI; 2004-348438/32.
XX
PTNew nucleic acid molecule for diagnosing, preventing or treating diseases
PTsuch as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PTgenetic, bacterial and viral diseases.
XX
PSClaim 1; SEQ ID NO 3472; 428pp; English.
XX
CCThe present invention relates to an isolated nucleic acid molecule
CCencoding a polypeptide which is believed to be cytostatic,
CCantiinflammatory, immunosuppressive, antibacterial and virucidal. The
CCcomposition and methods are useful for diagnosing, preventing and
CCtreating diseases such as proliferative (e.g. cancer), inflammatory,
CCimmune, metabolic, genetic, bacterial and viral diseases. The present
CCsequence represents a human secreted protein. The present sequence is
CCavailable on WIPOWEB and is not in the specification.
XX
SQSequence 144 AA;

Query Match 100.0%; Score 18; DB 8; Length 144;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY1 CXXXXXXXXC 10
|
Db72 CAATAAATC 81

RESULT 8
ABO69151
ID ABO69151 standard; protein; 167 AA.
XX
AC ABO69151;
XX
DT29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #1326.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.

XX22-APR-2003.
PD
XX
PF18-FEB-1999; 99US-00252991.
XX
PR18-FEB-1998; 98US-0074788P.
PR27-JUL-1998; 98US-0094190P.
XX
PA(GENO-) GENOME THERAPEUTICS CORP.
XX
PIRubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DRWPI; 2003-615309/58.
DRN-PSDB; ABD02722.
XX
PTNovel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PTuseful as molecular targets for diagnostics, prophylaxis and treatment of
PTpathological conditions resulting from bacterial infection.
XX
PSDisclosure; SEQ ID NO 17897; 455pp; English.
XX
CCThe invention relates to Pseudomonas aeruginosa polypeptides and the
CCpolynucleotides encoding them. The sequences are useful in diagnosis and
CCtherapy of pathological conditions, as molecular targets for diagnostics,
CCprophylaxis and treatment of pathological conditions resulting from a
CCbacterial infection, for evaluating a compound, such as a polypeptide,
CCfor the ability to bind a P. aeruginosa nucleic acid, as components of
CCeffective antibacterial targets, as targets for antibacterial drugs,
CCincluding anti-P. aeruginosa drugs, as templates for recombinant
CCproduction of P. aeruginosa-derived peptides or polypeptides, as target
CCcomponents for diagnosis and/or treatment of P. aeruginosa-caused
CCinfection, and in detection of P. aeruginosa sequences or other sequences
CCof Pseudomonas species using biochip technology. Sequences ABO67826-
CCABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CCsequence data for this patent did not form part of the printed
CCspecification but was obtained in electronic format from USPTO at
CCseqdata.uspto.gov/sequence.html
XX
SQSequence 167 AA;

Query Match 100.0%; Score 18; DB 7; Length 167;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY1 CXXXXXXXXC 10
|
Db60 CSTSTSTTSC 69

RESULT 9
ADS12185
ID ADS12185 standard; protein; 169 AA.
XX
AC ADS12185;
XX
DT16-DEC-2004 (first entry)
XX
DE Human therapeutic contig.protein - SEQ ID 2422.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
OS Homo sapiens.
XX
XX
FHKey Location/Qualifiers
FT Misc-difference 1. .169
FT /label= Unknown, OTHER
FT /note= "OTHER = In-frame STOP codon"
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.
PF
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y; Zhou P;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
DR WPI; 2004-668857/65.
DR N-PSDB; ADS11587.
XX
PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
PS Example 2; SEQ ID NO 2422; 718pp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC protein of the invention.
XX
SQ Sequence 169 AA;

Query Match 100.0%; Score 18; DB 8; Length 169;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
Db 81 CAAAAAAAC 90

RESULT 10
ADP30794
ID ADP30794 standard; protein; 171 AA.
XX
AC ADP30794;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human secreted protein SEQ ID #1561.
XX
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
PN WO2004035732-A2.
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DR WPI; 2004-348438/32.
XX
PT New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
PS Claim 1; SEQ ID NO 2792; 428pp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,

CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
SQ Sequence 171 AA;

Query Match 100.0%; Score 18; DB 8; Length 171;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXC 10
Db 146 CAAATAAAAC 155

RESULT 11
ADP30793
ID ADP30793 standard; protein; 171 AA.
XX
AC ADP30793;
XX 12-AUG-2004 (first entry)
XX Human secreted protein SEQ ID #1560.
DE Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX Homo sapiens.
OS
XX WO2004035732-A2.
PN
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
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PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.

PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DR WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
PS Claim 1; SEQ ID NO 2791; 428pp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
SQ Sequence 171 AA;

Query Match 100.0%; Score 18; DB 8; Length 171;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXC 10
Db 146 CAAATAAAAC 155

RESULT 12
ADP30806
ID ADP30806 standard; protein; 183 AA.
XX

XX WPI; 2003-615309/58.
DR N-PSDB; ABDI0190.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 25365; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 191 AA;

Query Match 100.0%; Score 18; DB 7; Length 191;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 49 CSTAASATSC 58

RESULT 14
ADZ56213
ID ADZ56213 standard; protein; 214 AA.

XX AC ADZ56213;

XX 30-JUN-2005 (first entry)

XX Human KIAA0779 splice variant clone CLN00149041.a, protein.

XX KIAA0779; gene expression; inflammation; antiinflammatory; cancer;
KW proliferation; neoplasm; cytostatic; immune disorder; immunomodulator;
KW metabolic disorder; metabolic; viral infection; virucide; infection.

XX Homo sapiens.

XX WO2005035569-A2.

XX 21-APR-2005.

XX 12-OCT-2004; 2004WO-US033408.

XX 10-OCT-2003; 2003US-0510612P.

XX (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Wong JGP, Hestir K, Collins ALT;

XX WPI; 2005-296268/30.

XX N-PSDB; ADZ56200, ADZ56231.

XX New isolated KIAA0779 nucleic acids and polypeptides, useful for
PT diagnosing, preventing and/or treating inflammatory, immune, viral
PT disorders and cancer, such as kidney, lung, ovarian, bladder, breast,
PT prostate and skin cancers.

XX
PS
XX
XX The invention relates to an isolated nucleic acid molecule comprising at
CC least one polynucleotide sequence (appearing as ADZ56196-ADZ56197,
CC ADZ56199-ADZ56200, ADZ56226-ADZ56227 and ADZ56230-ADZ56231), sequences
CC hybridizing to them under high stringency conditions, sequences having at
CC least 80% sequence identity to them, their complements or biologically
CC active fragments. The nucleic acids are splice variants of the human
CC KIAA0779 gene, encoding transmembrane domain protein(s). Also included
CC are a double-stranded isolated nucleic acid molecule comprising the
CC nucleic acid molecule cited above, a vector comprising the isolated
CC nucleic acid molecule cited above (and a promoter that regulates the
CC expression of the nucleic acid molecule), a recombinant host cell
CC comprising the nucleic acid molecule cited above, an isolated polypeptide
CC (comprising the encoded proteins or the non-transmembrane (TM) regions of
CC the proteins), a method of making a recombinant host cell, a method of
CC making a polypeptide, a method of determining the presence of the nucleic
CC acid molecule cited above in a sample, a method of determining the
CC presence of a specific antibody to the polypeptide of (4) in a sample, a
CC method of determining the presence of the polypeptide in a sample, an
CC antibody specifically binding to and/or interfering with the biological
CC activity of the nucleic acid molecule cited above (or the polypeptide or
CC its biologically active fragment), a composition comprising a
CC pharmaceutical carrier or excipient (and one or more active agents chosen
CC from the nucleic acid molecule cited above, the vector, the polypeptide,
CC and the antibody), a bacteriophage comprising the antibody (or its
CC fragment), a bacterial cell comprising the bacteriophage, a recombinant
CC host cell that produces the antibody, an animal injected with one or more
CC active agents (chosen from the nucleic acid molecule, the vector, the
CC host cell, the polypeptide, and the antibody), a diagnostic kit
CC (comprising a nucleic acid molecule having at least 6 contiguous
CC nucleotides from the nucleic acid molecule cited above, the isolated
CC polypeptide, or antibody, and reagents to carry out an immunoassay), a
CC method of making an antibody, a method of identifying a modulating agent
CC that modulates the biological activity of the polypeptide, a modulator
CC composition comprising a modulator and a pharmaceutical carrier, a method
CC of treating a disease in a subject, and a method of treating cancer,
CC preferably kidney, cervical, squamous lung, ovarian, bladder, breast,
CC endometrial, prostate, and skin cancer, in a subject. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of inflammatory, immune, viral disorders and
CC cancer, such as kidney, cervical, squamous lung, ovarian, bladder,
CC breast, endometrial, prostate, and skin cancer. The present sequence
CC represents a protein encoded by a cDNA splice variant from the KIAA0779
CC gene.

XX SQ Sequence 214 AA;

Query Match 100.0%; Score 18; DB 9; Length 214;
Best Local Similarity 20.0%; Pred. No. 3.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 173 CAAAAAAAC 182

RESULT 15

ADP30921

ID ADP30921 standard; protein; 228 AA.

XX ADP30921;

XX 12-AUG-2004 (first entry)

XX Human secreted protein SEQ ID #1688.

XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX Homo sapiens.

```
PN WO2004035732-A2.
XX 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.
PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 14-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-048646P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR
XX 08-AUG-2003; 2003US-0493577P.
XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI Williams LT, Chu X, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DR WPI; 2004-348438/32.
XX
PT New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
PS Claim 1; SEQ ID NO 2919; 428pp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 18; DB 8; Length 228;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXXC 10
Db 54 CATAAATTAC 63
Search completed: May 2, 2006, 08:54:55
Job time : 113.791 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 18.1395 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	313	2 S59448	hypothetical prote
2	18	100.0	480	2 E75433	hypothetical prote
3	17	94.4	194	2 JQ1560	hypothetical 20.6K
4	17	94.4	220	2 JC4082	coat protein - Cym
5	17	94.4	376	2 AB2920	cobalamin biosynth
6	17	94.4	388	2 C97694	cobalamin biosynth
7	17	94.4	389	2 T23167	hypothetical prote
8	17	94.4	570	2 T37314	probable kexin (EC
9	17	94.4	634	2 S33575	dnaK-type molecula
10	17	94.4	942	2 D87803	protein bli-4D [im
11	17	94.4	2704	2 S09118	G surface protein
12	16	88.9	71	2 F84312	hypothetical prote
13	16	88.9	85	2 E70531	hypothetical prote
14	16	88.9	104	2 S51479	drought-induced pr
15	16	88.9	105	2 A71249	hypothetical prote
16	16	88.9	108	2 F72549	hypothetical prote
17	16	88.9	126	2 A23473	chymotrypsin-like
18	16	88.9	129	2 T49498	hypothetical prote
19	16	88.9	133	2 A96746	hypothetical prote
20	16	88.9	147	2 S09762	hypothetical prote
21	16	88.9	153	2 PN0103	hypothetical 17K p
22	16	88.9	161	2 T28088	hypothetical prote
23	16	88.9	164	2 JQ1252	hypothetical 16.7K
24	16	88.9	229	2 T34277	hypothetical prote
25	16	88.9	242	2 A45724	pectate lyase (EC
26	16	88.9	244	2 S72219	chymotrypsin B - A
27	16	88.9	251	2 A55035	cysteine-rich prot
28	16	88.9	262	1 JQ1724	E1 membrane glycop
29	16	88.9	263	2 S47537	chymotrypsin (EC 3

30	16	88.9	275	2 A85856	probable elongatio
31	16	88.9	275	2 B64986	hypothetical 30.9
32	16	88.9	275	2 C91011	probable elongatio
33	16	88.9	294	2 T23682	hypothetical prote
34	16	88.9	306	2 C71498	probable yop trans
35	16	88.9	317	2 T00500	probable elicitor
36	16	88.9	321	2 A84792	hypothetical prote
37	16	88.9	349	2 JE0202	paired-box-contain
38	16	88.9	380	2 T04007	hypothetical prote
39	16	88.9	397	2 T26077	hypothetical prote
40	16	88.9	422	2 S41514	RAD52 protein homo
41	16	88.9	473	2 C81039	lipopolysaccharide
42	16	88.9	473	2 C81984	probable lipopolys
43	16	88.9	475	2 T36342	probable glutamate
44	16	88.9	486	2 B86460	hypothetical prote
45	16	88.9	510	2 A55207	glycerol-3-phospha

ALIGNMENTS

RESULT 1

S59448
hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YMR325.07
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59448
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59441
A;Accession: S59448
A;Molecule type: DNA
A;Residues: 1-313 <ODE>
A;Cross-references: UNIPROT:Q03695; UNIPARC:UPI000013B90A; EMBL:Z48755; NID:g736296; P
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR206w
A;Cross-references: SGD:S0004819
A;Map position: 13R

Query Match 100.0%; Score 18; DB 2; Length 313;
Best local Similarity 20.0%; Pred. No. 0.44;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 245 CSSSSSSSSSAC 254

RESULT 2

E75433
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75433
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75433
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <WHI>
A;Cross-references: UNIPROT:Q9RV87; UNIPARC:UPI00000C18A8; GB:AE001963; GB:AE000513; P
A;Experimental source: strain R1
C;Genetics:

A;Gene: DR1142
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR1142

Query Match 100.0%; Score 18; DB 2; Length 480;
Best Local Similarity 20.0%; Pred. NO. 0.51;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 464 CASAAATAAC 473

RESULT 3
JQ1560
hypotheical 20.6K protein - Lymantria dispar nuclear polyhedrosis virus
N;Alternate names: hypothetical protein 4
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1560
R;Bjornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria dispar nuclear polyhedrosis virus
A;Reference number: PQ0339; MUID:92300345; PMID:1607868
A;Accession: JQ1560
A;Molecule type: DNA
A;Residues: 1-194 <BJO>
A;Cross-references: UNIPROT:P36868; UNIPARC:UPI000017A7BF; DDBJ:D10836

Query Match 94.4%; Score 17; DB 2; Length 194;
Best Local Similarity 20.0%; Pred. NO. 1.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 74 CSAAMTSSC 83

RESULT 4
JC4082
coat protein - Cymbidium mosaic virus
C;Species: Cymbidium mosaic virus
C;Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: JC4082
R;Ryu, K.H.; Yoon, K.E.; Park, W.M.
Gene 156, 303-304, 1995
A;Title: Cloning and sequencing of a cDNA encoding the coat protein of a Korean isolate
A;Reference number: JC4082; MUID:95278762; PMID:7758973
A;Accession: JC4082
A;Molecule type: mRNA
A;Residues: 1-220 <RYU>
A;Cross-references: UNIPROT:Q66152; UNIPARC:UPI00000F22DE; EMBL:X81051; NID:9897718; PID:9897718
A;Note: The authors translated the codon GTG for residue 161 as Leu
C;Superfamily: potato virus coat protein
C;Keywords: coat protein

Query Match 94.4%; Score 17; DB 2; Length 220;
Best Local Similarity 20.0%; Pred. NO. 1.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 166 CSAATLTATC 175

RESULT 5
AB2920
cobalamin biosynthetic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2920
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, G.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <KUR>
A;Cross-references: UNIPROT:Q8UBQ6; UNIPARC:UPI0000164772; GB:AE008688; PIDN:AAI43776.
A;Experimental source: strain C58 (Dupont)
C;Genetics:

A;Gene: cbid
A;Map position: circular chromosome
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D

Query Match 94.4%; Score 17; DB 2; Length 376;
Best Local Similarity 20.0%; Pred. NO. 2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 17 CAAATKAAC 26

RESULT 6

C97694
cobalamin biosynthetic protein cbid (PA2908) [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97694
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldma; A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: UNIPROT:Q8UBQ6; UNIPARC:UPI00000D2014; GB:AE007869; PIDN:AAK88508.
C;Genetics:

A;Gene: AGR_C_5073
A;Map position: circular chromosome
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D

Query Match 94.4%; Score 17; DB 2; Length 388;
Best Local Similarity 20.0%; Pred. NO. 2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 29 CAAATKAAC 38

RESULT 7

T23167
hypothetical protein K01C8.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23167

R;Sims, M.
submitted to the EMBL Data Library, April 1995

A;Reference number: Z19702
A;Accession: T23167

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

A;Residues: 1-389 <WIL>

A;Cross-references: UNIPROT:Q21081; UNIPARC:UPI0000080155; EMBL:Z49068; PIDN:CAA88855.
A;Experimental source: clone K01C8

C;Genetics:

A;Gene: CESP:K01C8.2

A;Map position: 2

A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3

Query Match 94.4%; Score 17; DB 2; Length 389;

Best Local Similarity 20.0%; Pred. No. 2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 123 CSSSISTSSC 132

RESULT 8
T37314
probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)
N;Alternate names: blisterase 4
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T37314
R;Thacker, C.; Peters, K.; Srayko, M.; Rose, A.M.
Genes Dev. 9, 956-971, 1995
A;Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su
A;Reference number: Z21679; MUID:95293228; PMID:7774813
A;Accession: T37314
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-570 <THA>
A;Cross-references: UNIPARC:UPI000016B8E1; EMBL:L29440; NID:g459702; PIDN:AAA98752.1; PI
C;Genetics:
A;Gene: bli-4
A;Map position: 1
C;Keywords: alternative splicing; hydrolase; serine proteinase

Query Match 94.4%; Score 17; DB 2; Length 570;
Best Local Similarity 20.0%; Pred. No. 2.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 311 CTESSSATSC 320

RESULT 9
S33575
dnaK-type molecular chaperone precursor, mitochondrial - Leishmania major
N;Alternate names: heat shock protein 70-related protein; mitochondrial stress protein
C;Species: Leishmania major
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 31-Dec-2004
C;Accession: S33575; S78090; S05438
R;Searle, S.; McCrossan, M.V.; Smith, D.F.
J. Cell Sci. 104, 1091-1100, 1993
A;Title: Expression of a mitochondrial stress protein in the protozoan parasite Leishman
A;Reference number: S33575; MUID:93300981; PMID:8314893
A;Accession: S33575
A;Molecule type: DNA
A;Residues: 1-634 <SEA>
A;Cross-references: UNIPROT:P12076; UNIPARC:UPI0000177D24; EMBL:X64137
R;Smith, D.F.
submitted to the EMBL Data Library, January 1992
A;Reference number: S78090
A;Accession: S78090
A;Molecule type: DNA
A;Residues: 1-460, 481-500, 'QGEREIASENQIRGEFDLSG', 501-634 <SMI>
A;Cross-references: UNIPARC:UPI000012CC5C; EMBL:X64137; NID:g311289; PIDN:CAA45498.1; PI
R;Searle, S.; Campos, A.J.R.; Coulson, R.M.R.; Spithill, T.W.; Smith, D.F.
Nucleic Acids Res. 17, 5081-5095, 1989
A;Title: A family of heat shock protein 70-related genes are expressed in the promastig
A;Reference number: S05438; MUID:89345072; PMID:2762121
A;Accession: S05438
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <SEF>
A;Cross-references: UNIPARC:UPI000016BF1C; EMBL:X14574; NID:g9561; PIDN:CAA32713.1; PID:
C;Genetics:
A;Gene: Lmhsp70.1
A;Genome: nuclear
C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein com
C;Superfamily: bcr protein
C;Keywords: ATP; mitochondrion; molecular chaperone; stress-induced protein
F;1-23/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;24-634/Product: heat shock protein 70, mitochondrial #status predicted <MAT>

Query Match 94.4%; Score 17; DB 2; Length 634;
Best Local Similarity 20.0%; Pred. No. 2.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 7 CGSAAASAAAC 16

RESULT 10
D87803
protein bli-4D [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: D87803
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_e
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a
A;Accession: D87803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-942 <STO>
A;Cross-references: UNIPARC:UPI000016B639; GB:chr_I; PIDN:AAB96754.1; PID:g2773243; GS
C;Genetics:
A;Gene: bli-4D
A;Map position: 1
C;Superfamily: kexin; subtilisin homology

Query Match 94.4%; Score 17; DB 2; Length 942;
Best Local Similarity 20.0%; Pred. No. 2.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 683 CTESSSATSC 692

RESULT 11
S09118
G surface protein 168 - Paramecium primaurelia
C;Species: Paramecium primaurelia
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09118
R;Prat, A.
J. Mol. Biol. 211, 521-535, 1990
A;Title: Conserved sequences flank variable tandem repeats in two alleles of the G sur
A;Reference number: S09118; MUID:90172419; PMID:2308165
A;Accession: S09118
A;Molecule type: DNA
A;Residues: 1-2704 <PRA>
A;Cross-references: UNIPROT:P17053; UNIPARC:UPI000012AE23; EMBL:X52133; NID:g10049; PI
C;Genetics:
A;Genetic code: SGC5
C;Superfamily: G surface protein

Query Match 94.4%; Score 17; DB 2; Length 2704;
Best Local Similarity 20.0%; Pred. No. 4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 1632 CVAATAATTC 1641

RESULT 12

F84312
hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84312
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84312
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <STO>
A;Cross-references: UNIPROT:Q9HPK1; UNIPARC:UPI0000063920; GB:AE004437; NID:GI0581076; P
C;Genetics:
A;Gene: VNG1598H

Query Match 88.9%; Score 16; DB 2; Length 71;
Best Local Similarity 20.0%; Pred. No. 4.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

Qy      1 CXXXXXXXXX 10
         |
Db      30 C S R S V S T S C 39

```

RESULT 13

E70531
hypothetical protein Rv2706c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: E70531
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70531
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-85 <COL>
A:Cross-references: UNIPROT:O07207; UNIPARC:UPI00000C14DC; GB:Z96072; GB:AL123456; NID:9
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2706c

Query Match 88.9%; Score 16; DB 2; Length 85;
Best Local Similarity 20.0%; Pred. No. 5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1	CXXXXXXC	10
D _b	24	CSATAVAAC	33

RESULT 14

S51479
drought-induced protein Di21 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S51479; S43176
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.
Mol. Gen. Genet. 246, 10-18, 1995
A;Title: Abscisic acid-dependent and -independent regulation of gene expression by progra
A;Reference number: S51478; MUID:95124290; PMID:7823904
A;Accession: S51479
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-104 <GOS>
A;Cross-references: UNIPROT:Q39084; UNIPARC:UPI000000BF21; EMBL:X75585; NID:g469111; P:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

A; Gene: **DIZ1**
C; Superfamily: **late embryogenesis-abundant protein lea5**

Query Match	88.9%;	Score 16;	DB 2;	Length 104;
Best Local Similarity	20.0%;	Pred. No. 5.4;		
Matches 2;	Conservative	0;	Mismatches	8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
db 14 CSAASGSLSC 23

RESULT 15

A71249
 hypothetical protein PH0248 - *Pyrococcus horikoshii*
 C;Species: *Pyrococcus horikoshii*
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C;Accession: A71249
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, N.
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: A71249
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-105 <KAW>
 A;Cross-references: UNIPROT:O57986; UNIPARC:UPI0000062D66; GB:AP000001; NID:G3236128;
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBan.
 C;Genetics:
 A;Gene: PH0248

Query Match 88.9%; Score 16; DB 2; Length 105;
Best Local Similarity 20.0%; Pred. No. 5.4;
Matches 2; Conservative 0; Mismatches 8; Indels

```

Qy      1 CXXXXXXXC 10
         |
Db     35 CFTASASLAC 44

```

Search completed: May 2, 2006, 08:56:19
Job time : 19.1395 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 113.256 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXXC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	100.0	213	2	Q96KM3 HUMAN	Q96km3 homo sapien
2	18	100.0	263	2	Q586F4_9TRYP	Q586f4 trypanosoma
3	18	100.0	269	2	Q7PRQ7_ANOGA	Q7prq7 anopheles g
4	18	100.0	281	2	Q5TX10_ANOGA	Q5tx10 anopheles g
5	18	100.0	313	1	YM58_YEAST	Q03695 saccharomyc
6	18	100.0	357	2	Q6ZDR4_ORYSA	Q6zdr4 oryza sativ
7	18	100.0	362	2	Q7QJL0_ANOGA	Q7qjl0 anopheles g
8	18	100.0	480	2	Q9RV87_DEIRA	Q9rv87 deinococcus
9	18	100.0	653	1	TMCC1_HUMAN	Q94876 homo sapien
10	18	100.0	1005	2	Q5H317_XANOR	Q5h317 xanthomonas
11	18	100.0	1061	2	Q4QCX7_LEIMA	Q4qcx7 leishmania
12	17	94.4	52	2	Q8LPD6_HORVU	Q8lpd6 hordeum vul
13	17	94.4	122	2	Q5DCN3_SCHJA	Q5dcn3 schistosoma
14	17	94.4	128	2	Q96LJ4_HUMAN	Q96lj4 homo sapien
15	17	94.4	139	2	Q6ZKM7_ORYSA	Q6zkm7 oryza sativ
16	17	94.4	155	2	Q6H482_ORYSA	Q6h482 oryza sativ
17	17	94.4	160	2	Q657M0_ORYSA	Q657m0 oryza sativ
18	17	94.4	160	2	Q4T4H1_TETNG	Q4t4h1 tetraodon n
19	17	94.4	219	2	Q825E8_STRAW	Q825e8 streptomyce
20	17	94.4	220	2	Q66152_9VIRU	Q66152 cymbidium m
21	17	94.4	256	2	Q6YTS2_ORYSA	Q6yts2 oryza sativ
22	17	94.4	260	2	Q850Z3_ORYSA	Q850z3 oryza sativ
23	17	94.4	304	2	Q5TVE4_ANOGA	Q5tve4 anopheles g
24	17	94.4	344	2	Q582B8_9TRYP	Q582b8 trypanosoma
25	17	94.4	361	2	Q57Z20_9TRYP	Q57z20 trypanosoma
26	17	94.4	364	2	Q4YW87_PLABE	Q4yw87 plasmodium
27	17	94.4	368	2	Q70RD3_GERHY	Q70rd3 gerbera hyb
28	17	94.4	376	1	CBID_AGR5	Q8ubq6 agrobacteri
29	17	94.4	388	2	Q7PYI3_ANOGA	Q7pyi3 anopheles g
30	17	94.4	389	2	Q21081_CAEEL	Q21081 caenorhabdi
31	17	94.4	411	2	Q67UZ3_ORYSA	Q67uz3 oryza sativ

32	17	94.4	437	2	Q4I4Q8_GIBZE	Q4i4q8 gibberella
33	17	94.4	471	2	Q9VMG7_DROME	Q9vmg7 drosophila
34	17	94.4	475	2	Q7X7A4_ORYSA	Q7x7a4 oryza sativ
35	17	94.4	491	2	Q4P4C7_USTMA	Q4p4c7 ustilago ma
36	17	94.4	520	2	Q4XZV5_PLACH	Q4xzv5 plasmodium
37	17	94.4	556	2	Q803D5_BRARE	Q803d5 brachydanio
38	17	94.4	568	2	Q5GXM1_XANOR	Q5gxml xanthomonas
39	17	94.4	626	2	Q4N2Y7_THEPA	Q4n2y7 theileria p
40	17	94.4	630	2	Q69TY8_ORYSA	Q69ty8 oryza sativ
41	17	94.4	634	1	HSP71_LEIMA	P12076 leishmania
42	17	94.4	635	2	Q4Q747_LEIMA	Q4q747 leishmania
43	17	94.4	652	2	Q4Q740_LEIMA	Q4q740 leishmania
44	17	94.4	660	2	Q4Q744_LEIMA	Q4q744 leishmania
45	17	94.4	662	2	Q4Q745_LEIMA	Q4q745 leishmania

ALIGNMENTS

RESULT 1
Q96KM3 HUMAN
ID Q96KM3_HUMAN PRELIMINARY; PRT; 213 AA.
AC Q96KM3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Aberrant WW domain-containing oxidoreductase.
GN Name=WWOX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21457335; PubMed=11572989; DOI=10.1073/pnas.191175898;
RA Paige A.J.W., Taylor K.J., Taylor C., Hillier S.G., Farrington S.,
RA Scott D., Porteous D.J., Smyth J.F., Gabra H., Watson J.E.V.;
RT "WWOX: a candidate tumor suppressor gene involved in multiple tumor
types.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:11417-11422 (2001).
DR EMBL; AF325432; AAL05451.1; -; Genomic_DNA.
DR EMBL; AF325423; AAL05451.1; JOINED; Genomic_DNA.
DR EMBL; AF325424; AAL05451.1; JOINED; Genomic_DNA.
DR EMBL; AF325426; AAL05451.1; JOINED; Genomic_DNA.
DR EMBL; AF325433; AAL05451.1; JOINED; Genomic_DNA.
DR EMBL; AF325425; AAL05451.1; JOINED; Genomic_DNA.
DR HSSP; Q13526; IPIN.
DR Ensembl; ENSG00000186153; Homo sapiens.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR Pfam; PF00397; WW; 2.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 213 AA; 23868 MW; A21054FF8214CC7C CRC64;

Query Match 100.0%; Score 18; DB 2; Length 213;
Best Local Similarity 20.0%; Pred. No. 0.43;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXC 10
Db 184 CTSTTTAAAC 193

RESULT 2
Q586F4_9TRYP
ID Q586F4_9TRYP PRELIMINARY; PRT; 263 AA.
AC Q586F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.

ORFNames=Tb927.6.4820;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008146; AAX80300.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 263 AA; 28873 MW; F61DFSAP910531AB CRC64;

Query Match 100.0%; Score 18; DB 2; Length 263;
Best Local Similarity 20.0%; Pred. No. 0.46;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 95 CATTSSSSAC 104

RESULT 3
Q7PRQ7 ANOGA
ID Q7PRQ7 ANOGA PRELIMINARY; PRT; 269 AA.
AC Q7PRQ7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001657 (Fragment).
GN ORFNames=ENSANGG0000001387;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAB01008847; EAA06779.3; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 269
SQ SEQUENCE 269 AA; 24228 MW; 25BBFF71FD71F1F2 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 269;
Best Local Similarity 20.0%; Pred. No. 0.47;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 149 CTSSSSTTSC 158

RESULT 4
Q5TX10 ANOGA
ID Q5TX10 ANOGA PRELIMINARY; PRT; 281 AA.
AC Q5TX10;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ENSANGP00000027669 (Fragment).
GN ORFNames=ENSANGG00000007023;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAB01008807; EAL41760.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 281
SQ SEQUENCE 281 AA; 25341 MW; 0462E1169FB8642B CRC64;

Query Match 100.0%; Score 18; DB 2; Length 281;
Best Local Similarity 20.0%; Pred. No. 0.48;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 107 CTAASSTAC 116

RESULT 5
YM58 YEAST
ID YM58 YEAST STANDARD; PRT; 313 AA.
AC Q03695;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 35.0 kDa protein in PFK2-HFA1 intergenic region.
GN OrderedLocusNames=YMR206W; ORFNames=YMR325.07;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII."
RL Nature 387:90-93(1997).
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; 248755; CAA88648.1; -; Genomic_DNA.
DR PIR; S59448; S59448.
DR GerMOnline; 142881; -.
DR Ensembl; YMR206W; Saccharomyces cerevisiae.
DR SGD; S000004819; YMR206W.
KW Complete proteome; Hypothetical protein.
FT COMPBIAS 3 6 Poly-Ser.
FT COMPBIAS 146 149 Poly-Gln.
FT COMPBIAS 246 252 Poly-Ser.
SQ SEQUENCE 313 AA; 35018 MW; 9D92BFDE982577F0 CRC64;

Query Match 100.0%; Score 18; DB 1; Length 313;
Best Local Similarity 20.0%; Pred. No. 0.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 245 CSSSSSSSSAC 254

RESULT 6
Q6ZDR4_ORYSA
ID Q6ZDR4_ORYSA PRELIMINARY; PRT; 357 AA.
AC Q6ZDR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transcription factor Myb protein.
GN Name=P0481F05.20;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
clone: P0481F05.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AP004376; BAD09322.1; -; Genomic_DNA.
DR HSSP; Q03237; 1A5J.
DR Gramene; Q6ZDR4; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR001005; Myb DNA_bd.
DR Pfam; PF00249; Myb DNA_binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
KW Nuclear protein; Repeat.
SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 357;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 322 CSATASASSC 331

RESULT 7
Q7QJL0_ANOGA
ID Q7QJL0_ANOGA PRELIMINARY; PRT; 362 AA.

AC Q7QJL0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000009383 (Fragment).
GN ORFNames=ENSANGG00000007023;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008807; EAA04378.2; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 362 AA; 32490 MW; 384376DDF431BEC0 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 362;
Best Local Similarity 20.0%; Pred. No. 0.52;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 187 CTAASSTAC 196

RESULT 8
Q9RV87_DEIRA
ID Q9RV87_DEIRA PRELIMINARY; PRT; 480 AA.
AC Q9RV87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR1142.
GN OrderedLocusNames=DR1142;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001963; AAF10716.1; -; Genomic_DNA.
DR PIR; E75433; E75433.
DR TIGR; DR1142; -.

Complete proteome; Hypothetical protein.
SEQUENCE 480 AA; 49364 MW; 18B962ADA5CA24AE CRC64;

Query Match 100.0%; Score 18; DB 2; Length 480;
Best Local Similarity 20.0%; Pred. No. 0.58;


```
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1 CXXXXXXXC 10
Db 464 CASAAATAAC 473

RESULT 9
TMCC1 HUMAN
ID TMCC1_HUMAN STANDARD; PRT; 653 AA.
AC O94876; Q68E06; Q8IXM8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Transmembrane and coiled-coil domains protein 1.
GN Name=TMCC1; Synonyms=KIAA0779;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 15-653.
RC TISSUE=Endometrial tumor;
RG The German cDNA consortium;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 334-653.
RC TISSUE=Brain;
RX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
CC -!- SIMILARITY: Belongs to the TEX28 family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB018322; BAA34499.1; -; mRNA.
CC EMBL; BC039859; AAH39859.1; -; mRNA.
CC EMBL; CR749206; CAH18064.2; -; mRNA.
CC Ensembl; ENSG00000172765; Homo sapiens.
CC HGNC; HGNC:29116; TMCC1.
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KW Coiled coil; Transmembrane.
FT TRANSMEM 592 612 Potential.
FT TRANSMEM 625 645 Potential.
FT COILED 228 313 Potential.
FT COILED 458 576 Potential.
SQ SEQUENCE 653 AA; 72053 MW; 18B07D171E874205 CRC64;

Query Match 100.0%; Score 18; DB 1; Length 653;
Best Local Similarity 20.0%; Pred. No. 0.65;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 173 CAAAAAAAC 182

RESULT 10
Q5H3I7_XANOR
ID Q5H3I7_XANOR PRELIMINARY; PRT; 1005 AA.
AC Q5H3I7;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Transcriptional regulator.
GN Name=acok; OrderedLocusNames=XO01230;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KXO85;
RX PubMed=15673718; DOI=10.1093/nar/gki206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
RT the bacterial blight pathogen of rice.";
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW74484.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:001711; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR000792; HTH_LuxR.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011717; TPR_4.
DR Pfam; PF00196; GerE; 1.
DR Pfam; PF00515; TPR_1; 2.
DR Pfam; PF07721; TPR_4; 1.
DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH_LuxR; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00421; HTH_LuxR; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00622; HTH_LUXR_FAMILY; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
DR Complete proteome.
KW SEQUENCE 1005 AA; 110791 MW; 662961379FD37B61 CRC64;

Query Match 100.0%; Score 18; DB 2; Length 1005;
Best Local Similarity 20.0%; Pred. No. 0.77;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 386 CASATTAAAC 395

RESULT 11
```

Q4QCX7_LEIMA
ID Q4QCX7_LEIMA PRELIMINARY; PRT; 1061 AA.
AC Q4QCX7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Kinesin heavy chain, putative.
GN ORFNames=LmjF20.0640;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005259; CAJ03791.1; -; Genomic DNA.
SQ SEQUENCE 1061 AA; 113930 MW; 2C69385D06371DCD CRC64;

Query Match 100.0%; Score 18; DB 2; Length 1061;
Best Local Similarity 20.0%; Pred. No. 0.79;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 192 CAATASTSC 201

RESULT 12
Q8LPD6_HORVU
ID Q8LPD6_HORVU PRELIMINARY; PRT; 52 AA.
AC Q8LPD6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative glutathione-S-transferase (Fragment).
GN Name=bar2;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baldwin A.;
RT "The effect of thiocarbamate herbicides and the safener dichlormid in
barley and wild oats.";
RL Thesis (2001), Department of Cardiff School of Biosciences, Cardiff
RL university, Cardiff, United Kingdom.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers H.J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ419772; CAD11963.1; -; mRNA.
DR HSSP; P12653; 1AXD.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR PRINTS; PR01590; HTHFIS.
KW Transferase.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5750 MW; 7392EB72A3C70B9B CRC64;

Query Match 94.4%; Score 17; DB 2; Length 52;
Best Local Similarity 20.0%; Pred. No. 1.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

Db 18 CTSASSTRSC 27

RESULT 13
Q5DCN3_SCHJA
ID Q5DCN3_SCHJA PRELIMINARY; PRT; 122 AA.
AC Q5DCN3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY814691; AAW26423.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 122 AA; 13028 MW; 960E8615986958DE CRC64;

Query Match 94.4%; Score 17; DB 2; Length 122;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 76 CTESSSTSC 85

RESULT 14
Q96LJ4_HUMAN
ID Q96LJ4_HUMAN PRELIMINARY; PRT; 128 AA.
AC Q96LJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ25437.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058166; BAB71697.1; -; mRNA.
DR Ensembl; ENSG00000178093; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
SQ SEQUENCE 128 AA; 14116 MW; D30AC8C668621B0C CRC64;

Query Match 94.4%; Score 17; DB 2; Length 128;
Best Local Similarity 20.0%; Pred. No. 1.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10

```
Db      118 CTATSSAKTC 127

RESULT 15
Q6ZKM7 ORYSA
ID Q6ZKM7_ORYSA PRELIMINARY; PRT; 139 AA.
AC Q6ZKM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OJ1118_A06.7-1.
GN Name=OJ1118_A06.7-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
RT clone:OJ1118_A06.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003873; BAD08805.1; -; Genomic_DNA.
DR Gramene; Q6ZKM7; -.
KW Hypothetical protein.
SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match      94.4%; Score 17; DB 2; Length 139;
Best Local Similarity 20.0%; Pred. No. 1.9;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXXC 10
Db      77 CAAITSSSSC 86

Search completed: May 2, 2006, 08:46:46
Job time : 116.256 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 93.0233 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	33	4	US-10-697-399-10
2	18	100.0	37	4	US-10-380-927-7
3	18	100.0	328	4	US-10-296-115-800
4	18	100.0	339	5	US-10-287-436A-231
5	18	100.0	356	5	US-10-450-763-51398
6	18	100.0	405	5	US-10-287-436A-216
7	18	100.0	429	4	US-10-424-955A-28
8	18	100.0	447	5	US-10-287-436A-206
9	18	100.0	465	5	US-10-287-436A-257
10	18	100.0	545	5	US-10-287-436A-271
11	18	100.0	598	4	US-10-437-963-162631
12	18	100.0	630	3	US-09-791-279-86
13	18	100.0	647	4	US-10-184-644-539
14	18	100.0	647	4	US-10-184-634-539
15	18	100.0	653	3	US-09-374-046A-20
16	18	100.0	653	4	US-10-102-524-1851
17	18	100.0	653	4	US-10-331-496A-81
18	18	100.0	653	4	US-10-616-263-20
19	18	100.0	693	4	US-10-123-155-499
20	18	100.0	693	4	US-10-146-731-499
21	18	100.0	693	4	US-10-140-472-499
22	18	100.0	693	4	US-10-141-761-499
23	18	100.0	693	4	US-10-142-885-499
24	18	100.0	693	4	US-10-158-790-499
25	18	100.0	693	4	US-10-137-871-499
26	18	100.0	693	4	US-10-140-923-499
27	18	100.0	693	4	US-10-141-756-499

28	18	100.0	693	4	US-10-141-759-499	Sequence 499, App
29	18	100.0	693	4	US-10-140-805-499	Sequence 499, App
30	18	100.0	693	4	US-10-140-864-499	Sequence 499, App
31	18	100.0	733	4	US-10-437-963-129702	Sequence 129702,
32	18	100.0	735	4	US-10-184-644-167	Sequence 167, App
33	18	100.0	735	4	US-10-184-634-167	Sequence 167, App
34	18	100.0	755	4	US-10-123-155-153	Sequence 153, App
35	18	100.0	755	4	US-10-146-731-153	Sequence 153, App
36	18	100.0	755	4	US-10-140-472-153	Sequence 153, App
37	18	100.0	755	4	US-10-141-761-153	Sequence 153, App
38	18	100.0	755	4	US-10-142-885-153	Sequence 153, App
39	18	100.0	755	4	US-10-158-790-153	Sequence 153, App
40	18	100.0	755	4	US-10-137-871-153	Sequence 153, App
41	18	100.0	755	4	US-10-140-923-153	Sequence 153, App
42	18	100.0	755	4	US-10-141-756-153	Sequence 153, App
43	18	100.0	755	4	US-10-141-759-153	Sequence 153, App
44	18	100.0	755	4	US-10-140-805-153	Sequence 153, App
45	18	100.0	755	4	US-10-140-864-153	Sequence 153, App

ALIGNMENTS

RESULT 1
US-10-697-399-10
; Sequence 10, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-697-399-10

Query Match 100.0%; Score 18; DB 4; Length 33;
Best Local Similarity 20.0%; Pred.No. 2.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
Db 24 CTATTAAAC 33

RESULT 2 -
US-10-380-927-7
; Sequence 7, Application US/10380927
; Publication No. US20040110165A1
; GENERAL INFORMATION:
; APPLICANT: Larry W. Kwak
; APPLICANT: Arya Biragyn
; TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS
; FILE REFERENCE: 14014.0381U2
; CURRENT APPLICATION NUMBER: US/10/380,927
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/US01/29075
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,067
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence = Note
; OTHER INFORMATION: Synthetic Construct
US-10-380-927-7

Query Match 100.0%; Score 18; DB 4; Length 37;
Best Local Similarity 20.0%; Pred. No. 2.3;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
Db 7 CTTTATTTC 16

RESULT 3
US-10-296-115-800
; Sequence 800, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 800
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(328)
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-800

Query Match 100.0%; Score 18; DB 4; Length 328;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
Db 63 CAAAAAAAC 72

RESULT 4
US-10-287-436A-231
; Sequence 231, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-231

Query Match 100.0%; Score 18; DB 5; Length 339;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
Db 314 CTTTAAAC 323

RESULT 5
US-10-450-763-51398
; Sequence 51398, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51398
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (116)...(136)
; OTHER INFORMATION: RIBOKINASE SIGNATURE domain identified by eMATRIX, accession
; OTHER INFORMATION: number PR00990B, p-value=8.425e-10, raw score of 12.32
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(356)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-51398

Query Match 100.0%; Score 18; DB 5; Length 356;
Best Local Similarity 20.0%; Pred. No. 3.4;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
|
Db 183 CAAAAAAASC 192

RESULT 6
US-10-287-436A-216
; Sequence 216, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-216

Query Match 100.0%; Score 18; DB 5; Length 405;

Best Local Similarity 20.0%; Pred. No. 3.5; Mismatches 8; Indels 0; Gaps 0;
Matches 2; Conservative 0;

QY 1 CXXXXXXXC 10
DB 340 CAAATAATC 349

RESULT 7

US-10-424-955A-28
; Sequence 28, Application US/10424955A
; Publication No. US20040014658A1
; GENERAL INFORMATION:
; APPLICANT: PROCHON BIOTECH LTD.
; APPLICANT: Bogin, Oren
; APPLICANT: Yayon, Avner
; APPLICANT: Adar, Rivka
; TITLE OF INVENTION: ACTIVE VARIANTS OF FGF WITH IMPROVED SPECIFICITY
; FILE REFERENCE: 139380 IL
; CURRENT APPLICATION NUMBER: US/10/424,955A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 139380 IL
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-424-955A-28

Query Match 100.0%; Score 18; DB 4; Length 429;
Best Local Similarity 20.0%; Pred. No. 3.5;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 397 CATTTTAC 406

RESULT 8

US-10-287-436A-206
; Sequence 206, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-206

Query Match 100.0%; Score 18; DB 5; Length 447;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 226 CAATAAAC 235

RESULT 9

US-10-287-436A-257
; Sequence 257, Application US/10287436A

Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-257

Query Match 100.0%; Score 18; DB 5; Length 465;
Best Local Similarity 20.0%; Pred. No. 3.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 445. CTAATAAAC 454

RESULT 10

US-10-287-436A-271
; Sequence 271, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 271
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-271

Query Match 100.0%; Score 18; DB 5; Length 545;
Best Local Similarity 20.0%; Pred. No. 3.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 367 CTATTTTAC 376

RESULT 11

US-10-437-963-162631
; Sequence 162631, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162631
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61704C.1.pep
US-10-437-963-162631

Query Match 100.0%; Score 18; DB 4; Length 598;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 148 CTASSSSSSC 157

RESULT 12

US-09-791-279-86
; Sequence 86, Application US/09791279
; Publication No. US20030050456A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis
; APPLICANT: Lind, Peter
; TITLE OF INVENTION: No. US20030050456A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00048.US1
; CURRENT APPLICATION NUMBER: US/09/791,279
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,715
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184725
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,712
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,606
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,602
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,604
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,822
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,710
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,689
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,690
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,716
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-279-86

Query Match 100.0%; Score 18; DB 3; Length 630;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 128 CTTTTTAAC 137

RESULT 13

US-10-184-644-539
; Sequence 539, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 539
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-539

Query Match 100.0%; Score 18; DB 4; Length 647;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 288 CTTAAAAAAC 297

RESULT 14

US-10-184-634-539
; Sequence 539, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 539
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-539

Query Match 100.0%; Score 18; DB 4; Length 647;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10
Db 288 CTTAAAAAAC 297

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RESULT 15
US-09-374-046A-20
; Sequence 20, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (114)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (290)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (601)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (604)
;
US-09-374-046A-20

Query Match 100.0%; Score 18; DB 3; Length 653;
Best Local Similarity 20.0%; Pred. No. 3.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 173 CAAAAAAC 182

Search completed: May 2, 2006, 09:32:39
Job time : 94.0233 secs
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 14.186 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-33
Perfect score: 18
Sequence: 1 CXXXXXXXC 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	25	11	US-11-217-995-24 Sequence 24, Appl
2	18	100.0	36	11	US-11-174-341-161 Sequence 161, App
3	18	100.0	370	11	US-11-217-995-37 Sequence 37, Appl
4	18	100.0	407	11	US-11-079-463-10130 Sequence 10130, A
5	18	100.0	1197	11	US-11-178-230-10 Sequence 10, Appl
6	18	100.0	1886	9	US-10-515-868-8 Sequence 8, Appli
7	18	100.0	1894	9	US-10-194-487-97 Sequence 97, Appl
8	18	100.0	1894	9	US-10-195-883-97 Sequence 97, Appl
9	18	100.0	1894	9	US-10-195-888-97 Sequence 97, Appl
10	18	100.0	1894	9	US-10-195-889-97 Sequence 97, Appl
11	18	100.0	1917	11	US-11-241-631-5 Sequence 5, Appli
12	18	100.0	4440	9	US-10-194-487-525 Sequence 525, App
13	18	100.0	4440	9	US-10-195-883-525 Sequence 525, App
14	18	100.0	4440	9	US-10-195-888-525 Sequence 525, App
15	18	100.0	4440	9	US-10-195-889-525 Sequence 525, App
16	17	94.4	211	11	US-11-172-740-1547 Sequence 1547, Ap
17	17	94.4	228	9	US-10-980-388-17 Sequence 17, Appl
18	17	94.4	273	11	US-11-070-080-19 Sequence 19, Appl
19	17	94.4	296	11	US-11-182-343-31 Sequence 31, Appl
20	17	94.4	339	11	US-11-096-568A-19359 Sequence 19359, A
21	17	94.4	354	9	US-10-478-345-2 Sequence 2, Appli

22	17	94.4	381	11	US-11-096-568A-19358 Sequence 19358, A
23	17	94.4	382	11	US-11-217-995-38 Sequence 38, Appl
24	17	94.4	383	11	US-11-096-568A-19357 Sequence 19357, A
25	17	94.4	639	9	US-10-915-002-247 Sequence 247, App
26	17	94.4	1076	9	US-10-131-826A-219 Sequence 219, App
27	17	94.4	1076	9	US-10-973-115B-219 Sequence 219, App
28	17	94.4	1076	9	US-10-137-873A-219 Sequence 219, App
29	17	94.4	1076	9	US-10-152-370-219 Sequence 219, App
30	17	94.4	1076	11	US-11-290-153-219 Sequence 219, App
31	17	94.4	1141	11	US-11-217-995-35 Sequence 35, Appl
32	17	94.4	1141	11	US-11-217-995-36 Sequence 36, Appl
33	17	94.4	1300	9	US-10-194-487-269 Sequence 269, App
34	17	94.4	1300	9	US-10-195-883-269 Sequence 269, App
35	17	94.4	1300	9	US-10-195-888-269 Sequence 269, App
36	17	94.4	1300	9	US-10-195-889-269 Sequence 269, App
37	17	94.4	1356	9	US-10-894-592-3 Sequence 3, Appli
38	17	94.4	1503	11	US-11-145-405B-5 Sequence 5, Appli
39	17	94.4	1652	11	US-11-241-631-1 Sequence 1, Appli
40	17	94.4	1743	9	US-10-194-487-451 Sequence 451, App
41	17	94.4	1743	9	US-10-195-883-451 Sequence 451, App
42	17	94.4	1743	9	US-10-195-888-451 Sequence 451, App
43	17	94.4	1743	9	US-10-195-889-451 Sequence 451, App
44	17	94.4	2508	11	US-11-241-631-7 Sequence 7, Appli
45	17	94.4	2544	11	US-11-241-631-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-11-217-995-24
; Sequence 24, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
; APPLICANT: Robert Shields
; APPLICANT: Lawren Wu
; TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEPTOR ANTIBODY AND USES THEREFOR.
; FILE REFERENCE: P1935R1
; CURRENT APPLICATION NUMBER: US/11/217,995
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 60/606,851
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 24
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-217-995-24

Query Match 100.0%; Score 18; DB 11; Length 25;
Best Local Similarity 20.0%; Pred. No. 9e-05;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|
Db 1 CAATTATTTC 10

RESULT 2
US-11-174-341-161
; Sequence 161, Application US/11174341
; Publication No. US20060031967A1
; GENERAL INFORMATION:
; APPLICANT: Slade, Ann
; APPLICANT: Madisen, Linda
; APPLICANT: Comai, Luca
; TITLE OF INVENTION: Compositions and Methods for Modulation of Plant Cell
; TITLE OF INVENTION: Division
; FILE REFERENCE: 6769*2
; CURRENT APPLICATION NUMBER: US/11/174,341

; CURRENT FILING DATE: 2005-07-01
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 161
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Plant
US-11-174-341-161

Query Match 100.0%; Score 18; DB 11; Length 36;
Best Local Similarity 20.0%; Pred. No. 9.9e-05;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
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DB 19 CATTATAATC 28

RESULT 3

US-11-217-995-37
; Sequence 37, Application US/11217995
; Publication No. US20060073142A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Chan
; APPLICANT: Robert Shields
; APPLICANT: Lauren Wu
; TITLE OF INVENTION: ANTI-FC-GAMMA RIIB RECEPTOR ANTIBODY AND USES THEREFOR
; FILE REFERENCE: P1935R1
; CURRENT APPLICATION NUMBER: US/11/217,995
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 60/606,851
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-217-995-37

Query Match 100.0%; Score 18; DB 11; Length 370;
Best Local Similarity 20.0%; Pred. No. 0.00018;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|
DB 293 CATTATTAC 302

RESULT 4

US-11-079-463-10130
; Sequence 10130, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 10130
; LENGTH: 407
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-10130

Query Match 100.0%; Score 18; DB 11; Length 407;

Best Local Similarity 20.0%; Pred. No. 0.00018;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
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DB 5 CASATTSSAC 14

RESULT 5

US-11-178-230-10
; Sequence 10, Application US/11178230
; Publication No. US20060084162A1
; GENERAL INFORMATION:
; APPLICANT: Qasba, Pradman
; APPLICANT: Ramakrishnan, Boopathy
; APPLICANT: National Institutes of Health
; TITLE OF INVENTION: Catalytic Domains of (1,4)-Galactosyltransferase I Having Alter
; TITLE OF INVENTION: and Acceptor Specificities, Domains That Promote In Vitro Prote
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 1662.001US1
; CURRENT APPLICATION NUMBER: US/11/178,230
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/US2004/000470
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: US 60/439,298
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/450,250
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-230-10

Query Match 100.0%; Score 18; DB 11; Length 1197;
Best Local Similarity 20.0%; Pred. No. 0.00024;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
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DB 948 CATTTTAAAC 957

RESULT 6

US-10-515-868-8
; Sequence 8, Application US/10515868
; Publication No. US20050282729A1
; GENERAL INFORMATION:
; APPLICANT: Hamilton, David W
; APPLICANT: Roberts, Kenneth P
; APPLICANT: Ensrud, Kathy M
; TITLE OF INVENTION: CRISP POLYPEPTIDES AS CONTRACEPTIVES AND INHIBITORS OF SPERM
; TITLE OF INVENTION: CAPACITATION
; FILE REFERENCE: 110.01860101
; CURRENT APPLICATION NUMBER: US/10/515,868
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/383,628
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: PCT/US03/16669
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1886
; TYPE: PRT
; ORGANISM: HOMOSAPIEN
US-10-515-868-8

Query Match 100.0%; Score 18; DB 9; Length 1886;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|
Db 1359 CTATATATAC 1368

RESULT 7

US-10-194-487-97
; Sequence 97, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-97

Query Match 100.0%; Score 18; DB 9; Length 1894;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
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Db 1154 CAATTAAAC 1163

RESULT 8

US-10-195-883-97
; Sequence 97, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,883
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-97

Query Match 100.0%; Score 18; DB 9; Length 1894;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|
Db 1154 CAATTAAAC 1163

RESULT 9

US-10-195-888-97
; Sequence 97, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-888-97

Query Match 100.0%; Score 18; DB 9; Length 1894;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
|
Db 1154 CAATTAAAC 1163

RESULT 10

US-10-195-889-97
; Sequence 97, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C329
; CURRENT APPLICATION NUMBER: US/10/195,889
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 97
; LENGTH: 1894
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-889-97

Query Match      100.0%; Score 18; DB 9; Length 1894;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      1154 CAATTAAAC 1163

RESULT 11
US-11-241-631-5
; Sequence 5, Application US/11241631
; Publication No. US20060020115A1
; GENERAL INFORMATION:
; APPLICANT: Bamber, Bruce
; APPLICANT: Jorgensen, Erik
; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 21101.0009U4
; CURRENT APPLICATION NUMBER: US/11/241,631
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/10/156,240
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/436,063
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 60/107,727
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1917
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-241-631-5

Query Match      100.0%; Score 18; DB 11; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.00027;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      1049 CAAATATATC 1058

RESULT 12
US-10-194-487-525
; Sequence 525, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440.
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754

RESULT 13
US-10-195-883-525
; Sequence 525, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,883
; CURRENT FILING DATE: 2002-07-15
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-883-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754

FILE REFERENCE: P3430R1C329
CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 525
LENGTH: 4440
TYPE: PRT
ORGANISM: Homo Sapien
US-10-195-889-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754

Search completed: May 2, 2006, 09:33:44
Job time : 15.186 secs
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-883-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754

RESULT 14
US-10-195-888-525
; Sequence 525, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-888-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-195-883-525

Query Match      100.0%; Score 18; DB 9; Length 4440;
Best Local Similarity 20.0%; Pred. No. 0.00034;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
Db      3745 CTAAATATC 3754

RESULT 15
US-10-195-889-525
; Sequence 525, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 112.791 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	ABP53932 VEGFR-3 b
2	54	75.0	10	5	ABP53931
3	50	69.4	10	5	ABP53968 VEGFR-3 b
4	47.5	66.0	304	7	ADC87481 Human GPC
5	47	65.3	25	7	ADC99638 Cancer-re
6	46	63.9	17	6	AAO26074 Fc region
7	46	63.9	17	8	ADJ50741 Human ser
8	46	63.9	136	8	ADM87650 Human EST
9	45	62.5	20	5	AAU90545 Insulin/i
10	45	62.5	129	2	AAY59880 Human nor
11	45	62.5	828	6	ABU49938 Protein e
12	44.5	61.8	1024	5	ABB04861 LDL recep
13	44	61.1	112	9	AEA18628 Amino aci
14	44	61.1	119	9	AEA18657 Amino aci
15	44	61.1	119	9	AEA18667 Amino aci
16	44	61.1	119	9	AEA18683 Amino aci
17	44	61.1	119	9	AEA18679 Amino aci
18	44	61.1	119	9	AEA18675 Amino aci
19	44	61.1	119	9	AEA18661 Amino aci
20	44	61.1	119	9	AEA18665 Amino aci
21	44	61.1	119	9	AEA18671 Amino aci
22	44	61.1	119	9	AEA18687 Amino aci
23	44	61.1	119	9	AEA18689 Amino aci
24	44	61.1	119	9	AEA18659 Amino aci

25	44	61.1	119	9	AEA18681	Aeal18681 Amino aci
26	44	61.1	119	9	AEA18685	Aeal18685 Amino aci
27	44	61.1	119	9	AEA18669	Aeal18669 Amino aci
28	44	61.1	119	9	AEA18677	Aeal18677 Amino aci
29	44	61.1	119	9	AEA18691	Aeal18691 Amino aci
30	44	61.1	119	9	AEA18697	Aeal18697 Amino aci
31	44	61.1	119	9	AEA18673	Aeal18673 Amino aci
32	44	61.1	119	9	AEA18693	Aeal18693 Amino aci
33	44	61.1	119	9	AEA18699	Aeal18699 Amino aci
34	44	61.1	119	9	AEA18695	Aeal18695 Amino aci
35	44	61.1	119	9	AEA18663	Aeal18663 Amino aci
36	44	61.1	149	8	ADP29850	Adp29850 Human sec
37	44	61.1	166	6	AAE31487	Aae31487 Human but
38	44	61.1	415	5	AAU91293	Aau91293 Human NOV
39	44	61.1	468	9	AEA18640	Aeal18640 Amino aci
40	43	59.7	13	6	AAO26093	Aao26093 Fc region
41	43	59.7	13	8	ADJ50760	Adj50760 Human ser
42	43	59.7	291	8	ADS30280	Ads30280 Bacterial
43	43	59.7	454	5	ABP73979	Abp73979 Candida a
44	43	59.7	474	6	ABU30004	Abu30004 Protein e
45	43	59.7	492	7	ADC97318	Adc97318 E. faeciu

ALIGNMENTS

RESULT 1
ABP53932
ID ABP53932 standard; peptide; 10 AA.
XX
AC ABP53932;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:35.
XX

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
vulnery; cell surface receptor; cancer; neovascularisation;
liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
diabetes; PDGF; platelet derived growth factor.

Homo sapiens.
OS Synthetic.

PN WO200257299-A2.

XX 25-JUL-2002.

PF 16-JAN-2002; 2002WO-IB0000099.

PR 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.

XX Claim 13; Page 80; 149pp; English.

PS The present invention describes an isolated peptide (I) that binds to and
XX inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver; spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 72; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
Db 1 CGYWLTIWGC 10

RESULT 2
ABP53931
ID ABP53931 standard; peptide; 10 AA.
XX
AC ABP53931;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:34.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytotactic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "any amino acid"
FT Misc-difference 10 /note= "any amino acid"
FT
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 12; Page 80; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 75.0%; Score 54; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
Db 2 GYWLTIWG 9

RESULT 3
ABP53968
ID ABP53968 standard; peptide; 10 AA.
XX
AC ABP53968;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:73.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytotactic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5.7 /note= "X is any amino acid"
FT Misc-difference 9 /note= "X is any amino acid"
FT
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Disclosure; Page 147; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of

CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a VEGFR-3 binding peptide, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
||| |
Db 1 CGYWXXXWXC 10

RESULT 4
ADC87481
ID ADC87481 standard; protein; 304 AA.
XX
AC ADC87481;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR protein SEQ ID NO:1934.
XX
KW human; GPCR; guanosine triphosphate-binding protein coupled receptor;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI; 2003-315783/31.
DR N-PSDB; ADC87480.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 2; SEQ ID NO 1934; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
SQ Sequence 304 AA;

Query Match 66.0%; Score 47.5; DB 7; Length 304;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10
||| :|||

Db 108 CGFW-AVWGC 116

RESULT 5
ADC99638
ID ADC99638 standard; peptide; 25 AA.
XX
AC ADC99638;
XX
DT 01-JAN-2004 (first entry)
XX
DE Cancer-related Tie-1-binder peptide - SEQ ID 476.
XX
KW cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
KW leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
KW kinase insert domain protein receptor; EGFR; epidermal growth factor;
KW FGFR1; fibroblast growth factor; Tie-1.
XX
OS Unidentified.
XX
PN WO2003035839-A2.
XX
PD 01-MAY-2003.
XX
PF 24-OCT-2002; 2002WO-US034021.
XX
PR 24-OCT-2001; 2001US-0345471P.
XX
PA (DGI-) DGI BIOTECHNOLOGIES INC.
XX
PI Pillutla RC, Brissette R, Spruyt M, Dedova O, Blume A;
PI Prendergast J, Goldstein N;
XX
DR WPI; 2003-457332/43.
XX
PT Selecting target and target binder pairs for preparing a composition for
PT treating cancer by mixing in a reaction vessel phage expressing
PT biological targets and phage expressing target binders.
XX
PS Claim 26; SEQ ID NO 476; 172pp; English.
XX
CC The invention relates to a novel method of selecting target and target
CC binder pairs comprising mixing in a reaction vessel phage expressing
CC biological targets and phage expressing target binders, each having
CC distinguishable selection markers and selecting target and target binder
CC pairs based on the selection markers. The molecules of the invention
CC demonstrate cytostatic activity whilst the method may be useful for
CC selecting target and target binder pairs for preparing a composition for
CC treating cancer. Furthermore, the method may be utilised during gene
CC therapy procedures. The current sequence is that of the cancer-related
CC Tie1-binder peptide of the invention.
XX
SQ Sequence 25 AA;

Query Match 65.3%; Score 47; DB 7; Length 25;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9
||| :||
Db 5 CGYWGELWG 13

RESULT 6
AAO26074
ID AAO26074 standard; peptide; 17 AA.
XX
AC AAO26074;
XX
DT 03-APR-2003 (first entry)
XX
DE Fc region binding peptide SEQ ID No 54.

XX Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
KW antibody response; half-life; stability; circulatory system.
XX Unidentified.
OS WO200286070-A2.
XX 31-OCT-2002.
PD 18-APR-2002; 2002WO-US012492.
XX 18-APR-2001; 2001US-0284534P.
XX (DYAX-) DYAX CORP.
XX Rondon IJ, Wu Q, Ley AC, Stochl M, Ranschoff TC, Potter MD;
PI WPI; 2003-201220/19.
XX New polypeptides, useful as binding molecules for detecting, isolating or
PT purifying immunoglobulin Fc-region polypeptides present in a solution, or
PT for regulating or preventing an antibody response.
XX Claim 3; Page 76; 152pp; English.
PS The invention relates to novel isolated polypeptides comprising a
XX sequence that binds an immunoglobulin Fc region. The polypeptides are
CC useful as binding molecules for detecting, isolating or purifying
CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole
CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are
CC also useful for regulating or preventing an antibody response, or for
CC increasing the half-life and over all stability of a therapeutic or
CC diagnostic compound that is administered to or enters the circulatory
CC system of an individual. This sequence represents an Fc region binding
CC peptide of the invention
XX
SQ Sequence 17 AA;

Query Match 63.9%; Score 46; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9
Db 4 CGFWPRIWG 12

RESULT 7
ADJ50741
ID ADJ50741 standard; peptide; 17 AA.
XX
AC ADJ50741;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human serum albumin binding peptide, Seq ID No 278.
XX
KW human serum albumin; HSA; serum; blood; tumour; human.
XX
OS Homo sapiens.
XX
PN WO2003106493-A1.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-US018896.
XX
PR 14-JUN-2002; 2002US-0388642P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Sato AK, Dawson BM;

XX WPI; 2004-082161/08.
XX Evaluating sample comprising soluble serum protein by forming complex
PT comprising serum protein and physically associated compounds using
PT peptide ligand that specifically binds with proteins, which is separated
PT and evaluated.
XX
PS Disclosure; SEQ ID NO 278; 191pp; English.
XX
CC The invention relates to a method of evaluating sample by providing a
CC soluble serum protein (I), one or more compounds physically associated
CC with (I), and a (I)-binding agent that comprises a peptide that
CC specifically binds to (I), allowing the (I)-binding agent to bind to (I)
CC to form a complex including one or more compounds physically associated
CC with (I), separating the complex from one or more components of the
CC sample, and evaluating one or more of the physically associated
CC compounds. The sample comprises blood or serum, or is obtained from a
CC biopsy. The sample may also be obtained from a tumour or a region within
CC 5 mm of a tumour. The method is useful for detecting modulators that
CC modulate interaction of serum protein-binding compound and serum protein
CC and for identifying binding ligands for serum protein. The present
CC sequence represents a serum albumin-binding peptide identified using the
CC method of the invention.
XX
SQ Sequence 17 AA;

Query Match 63.9%; Score 46; DB 8; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9
Db 4 CGFWPRIWG 12

RESULT 8
ADM87650
ID ADM87650 standard; protein; 136 AA.
XX
AC ADM87650;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human EST derived amino acid sequence SEQ ID NO:743.
XX
KW respiratory; cytostatic; antiarthritic; antiinflammatory;
KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;
KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KW inflammatory condition; arthritis; inflammatory bowel disease;
KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KW graft versus host disease; human; expressed sequence tag; EST.
XX
OS Homo sapiens.
XX
PN WO2004009834-A2.
XX
PD 29-JAN-2004.
XX
PF 19-JUL-2002; 2002WO-US022858.
XX
PR 21-JUL-2001; 2001US-0306971P.
PR 28-MAR-2002; 2002US-00112944.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX
DR WPI; 2004-143291/14.
DR N-PSDB; ADM87432.
XX

PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.

XX
XX
XX Example 2; SEQ ID NO 743; 591pp; English.

XX
XX
XX The present invention describes an isolated polynucleotide (I): (a)
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b),
CC which encodes a polypeptide with biological activity, where the
CC polynucleotide hybridises to (I) under stringent hybridisation conditions
CC or has greater than 99% sequence identity with (I). (I) has respiratory,
CC cytostatic, antiarthritic, antiinflammatory, gastrointestinal,
CC antibacterial, immunosuppressive, antidiabetic and antirheumatic
CC activities, and can be used in gene therapy. (I) can be used for
CC generating polynucleotides encoding chimeric or fusion proteins and
CC heterologous protein sequences. The polynucleotides can be used to
CC express recombinant protein for analysis, characterisation or therapeutic
CC use; as markers for tissues in which the corresponding protein is
CC preferentially expressed; as molecular weight markers on gels; as
CC chromosome markers or tags to identify chromosomes or to map related gene
CC positions; to compare with endogenous DNA sequences in patients to
CC identify potential genetic disorders; as probes to hybridise and discover
CC genes, related DNA sequences; as a source of information to derive PCR
CC primers for genetic fingerprinting; as a probe to subtract-out known
CC sequences in the process of discovering other novel polynucleotides; for
CC selecting and making oligomers for attachment to a gene chip or other
CC support, including for examination of expression patterns; to raise anti-
CC protein antibodies using DNA immunisation techniques; and as an antigen
CC to raise anti-DNA antibodies or elicit another immune response. The
CC polynucleotides and polypeptides can also be used as nutritional sources
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC source, as a nitrogen source or as a source of carbohydrates. The
CC polynucleotides and polypeptides can also be used treat cancer. The
CC compositions are useful for promoting better or faster closure of non-
CC healing wounds, for the generation and regeneration of tissues, for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents an
CC expressed sequence tag (EST) derived amino acid sequence from the present
CC invention. N.B. The sequences for this patent were obtained from the
CC USPTO web site from an equivalent US patent US20040048249A1.

XX
SQ Sequence 136 AA;

Query Match 63.9%; Score 46; DB 8; Length 136;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
|||:||||
Db 93 CGRWDWLWGC 102

RESULT 9
AAU90545
ID AAU90545 standard; peptide; 20 AA.
XX
AC AAU90545;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor-binding peptide #2501.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW ophthalmological; insulin; receptor; gene therapy; diabetes;
KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
XX
OS Synthetic.

XX WO200172771-A2.
XX
XX 04-OCT-2001.
XX
XX 29-MAR-2000; 2000WO-US008528.
XX
XX 29-MAR-2000; 2000WO-US008528.
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.
XX (NOVO) NOVO NORDISK AS.
XX
XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Raverą M, Hsiao K;
XX WPI; 2002-025774/03.
DR
XX Modulating insulin activity in mammalian cells, for treating e.g.
XX diabetes and tumors, comprises using peptides that bind to insulin or
PT insulin-like growth factor receptors.
PT
XX Disclosure; Fig 8-3; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or
CC IGF-1 receptor-binding peptides and related amino acid sequences of the
CC invention

XX
SQ Sequence 20 AA;

Query Match 62.5%; Score 45; DB 5; Length 20;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
|||:||||
Db 8 CGAWPTWNC 17

RESULT 10
AAY59880
ID AAY59880 standard; protein; 129 AA.
XX
AC AAY59880;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human normal uterus tissue derived protein 43.
XX
KW Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
KW EST; expressed sequence tag.
XX
OS Homo sapiens.
XX
PN DE19817946-A1.
XX
PD 21-OCT-1999.
XX
PF 17-APR-1998; 98DE-01017946.
XX
PR 17-APR-1998; 98DE-01017946.
XX

PA (META-) METAGEN GES GENOMFORSCHUNG.MBH.
XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
PI WPI; 1999-591956/51.
XX N-PSDB; AAZ41339.
DR New nucleic acid sequences expressed in normal uterine tissues, and
XX derived polypeptides, for treatment of uterine cancer and identification
PT of therapeutic agents.
PT Claim 23; Page 138; 154pp; German.
XX This invention describes novel cDNA sequences (A) highly expressed in
CC normal uterine tissue which can have anticancer and cytostatic activity
CC and can be used for gene therapy. (A) are used (i) for recombinant
CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)
CC are used (i) to identify agents suitable for treatment of uterine cancer;
CC (ii) directly for treating this form of cancer (including expression from
CC gene therapy vectors) and (iii) for generation of specific antibodies.
CC (A) are identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of expression patterns. This
CC allows a significantly longer fragment of the gene to be revealed, so
CC should reduce the number of failures associated with the fact that ESTs
CC from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AAY59838-Y59892 represent protein fragments encoded by
CC the human uterine tissue derived cDNA fragments represented in AAZ41325-
CC Z41385
XX
SQ Sequence 129 AA;
Query Match 62.5%; Score 45; DB 2; Length 129;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CGYWLTIW 8
| : ||| : |
Db 32 CSHWLTfVW 39
RESULT 11
ABU49938
ID ABU49938 standard; protein; 828 AA.
XX
AC ABU49938;
XX 19-JUN-2003 (first entry)
XX Protein encoded by prokaryotic essential gene #35465.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
KW Versinia pestis.
XX
OS WO200277183-A2.
XX
PN 03-OCT-2002.
PD
PF 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR

DR N-PSDB; ACA53808.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 77862; 1766pp; English.
PS The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 828 AA;
Query Match 62.5%; Score 45; DB 6; Length 828;
Best Local Similarity 58.3%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
Qy 1 CGYWLTI--WGC 10
| | | | : | | |
Db 372 CGLWLELLSWG 383
RESULT 12
ABB04861
ID ABB04861 standard; protein; 1024 AA.
XX
AC ABB04861;
XX 13-MAR-2002 (first entry)
DT
XX LDL receptor binding protein Na channel brain 3 SEQ ID NO:84.
DE Low density lipoprotein receptor binding protein; signal transduction;
XX LDL receptor binding protein; LDL receptor signalling pathway.
KW Synthetic.
KW WO200184159-A2.
OS
XX 08-NOV-2001.
XX 24-APR-2001; 2001WO-US013214.
PF
XX 01-MAY-2000; 2000US-00562737.
PR

XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX
XX Herz J, Gotthardt M;
XX
XX WPI; 2002-082855/11.
XX
XX Detecting stress that alters interaction of LDL receptor binding
XX polypeptide with LDL receptor interaction domain, comprises detecting
XX difference in stress-biased and unbiased interaction of peptide and
XX domain in a system.
XX
XX Disclosure; Page 148-150; 200pp; English.
XX
XX The present invention describes a method for detecting a stress that
XX alters a functional interaction of a low density lipoprotein (LDL)
XX receptor binding protein (I) with an LDL receptor interaction domain
XX (II). The method involves introducing a predetermined stress into a
XX system which provides a stress-biased physical interaction of (I) with
XX (II), where in the absence of the stress, the system provides an unbiased
XX interaction of (I) and (II), and detecting the stress-biased interaction
XX of (I) and (II), where a difference between BI and UI indicates that the
XX stress alters the interaction of (I) and (II). (I) is selected from
XX SEMCAP-1, JIP-1, PSD-95, JIP-2, Talin, OMP25, CAPON, PIP4,5 Kinase, Na
XX channel brain 3, Mint1, ICAP-1 and APC subunit 10. The method is useful
XX for detecting a stress that alters functional interaction of LDL receptor
XX binding polypeptide with LDL receptor interaction domain. The method is
XX useful for detecting and modulating signal transduction through LDL
XX receptors. ABB04778 to ABB04909 represent LDL receptor binding proteins
XX which are used in the exemplification of the present invention
XX
XX Sequence 1024 AA;
SQ

Query Match 61.8%; Score 44.5; DB 5; Length 1024;
Best Local Similarity 54.5%; Pred. No. 7.8e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
||:|:|:|:
Db 892 CGHWIETWDC 902

RESULT 13
AEA18628
ID AEA18628 standard; peptide; 112 AA.
XX
XX AEA18628;
AC
XX
DT 28-JUL-2005 (first entry)
XX
XX Amino acid sequence of variable heavy chain region of murine B-Ly1.
DE
XX
XX antigen binding molecule; Fc receptor; B-cell marker; CD20;
KW antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
KW hematological disease; immune disorder; neoplasm; heavy chain;
KW B-Ly1 antibody.
XX
XX Mus sp.
OS
XX
PN WO2005044859-A2.
XX
PD 19-MAY-2005.
XX
PF 05-NOV-2004; 2004WO-IB003896.
XX
PR 05-NOV-2003; 2003US-0517096P.
XX
XX (GLYC-) GLYCART BIOTECHNOLOGY AG.
PA (UMAN/) UMANA P.
PA (BRUE/) BRUENKER P.
PA (FERR/) FERRARA C.
PA (SUTE/) SUTER T.
PA (PUEN/) PUENTENER U.
PA

PA (MOES/) MOESSNER E.
XX
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX
XX WPI; 2005-347056/35.
XX N-PSDB; AEA18629.
XX
XX New polynucleotides and encoded antigen binding molecules with increased
XX Fc receptor binding affinity and effector function, useful for
XX diagnosing, preventing or treating B-cell proliferative disorders,
XX including B cell lymphoma.
XX
XX Claim 9; SEQ ID NO 1; 187pp; English.
XX
XX The specification describes antigen binding molecules with increased Fc
XX receptor binding affinity and effector function. These antigen binding
XX molecules may have modified glycosylation, and are especially specific
XX for human B-cell marker CD20. The invention is useful for diagnosing,
XX preventing or treating disorders or diseases treatable by B-cell
XX depletion, such as B cell lymphoma. The present sequence represents the
XX variable heavy chain region of the murine antibody B-Ly1, and antibody
XX which binds CD20. The sequence is used to produce antigen binding
XX molecules of the invention.
XX
XX Sequence 112 AA;
SQ

Query Match 61.1%; Score 44; DB 9; Length 112;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|||||:
Db 96 GYWLTVWG 103

RESULT 14
AEA18657
ID AEA18657 standard; protein; 119 AA.
XX
XX AEA18657;
AC
XX
DT 28-JUL-2005 (first entry)
XX
XX Amino acid sequence of CD20 antigen binding molecule #1.
DE
XX
XX antigen binding molecule; Fc receptor; B-cell marker; CD20;
KW antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
KW hematological disease; immune disorder; neoplasm.
XX
XX Mus sp.
OS
XX Homo sapiens.
OS Chimeric.
XX
XX WO2005044859-A2.
PN
XX
PD 19-MAY-2005.
XX
XX 05-NOV-2004; 2004WO-IB003896.
PF
XX
PR 05-NOV-2003; 2003US-0517096P.
XX
XX (GLYC-) GLYCART BIOTECHNOLOGY AG.
PA (UMAN/) UMANA P.
PA (BRUE/) BRUENKER P.
PA (FERR/) FERRARA C.
PA (SUTE/) SUTER T.
PA (PUEN/) PUENTENER U.
PA (MOES/) MOESSNER E.
XX
XX Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
PI
XX
XX WPI; 2005-347056/35.
XX N-PSDB; AEA18656.
DR

XX New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function, useful for
PT diagnosing, preventing or treating B-cell proliferative disorders,
PT including B cell lymphoma.
XX Claim 128; SEQ ID NO 30; 187pp; English.
XX
CC The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents an
CC antigen binding molecule of the invention.
XX
SQ Sequence 119 AA;
Query Match 61.1%; Score 44; DB 9; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTIWG 9
Db 103 GYWLVIWG 110
RESULT 15
AEA18667
ID AEA18667 standard; protein; 119 AA.
XX
AC AEA18667;
XX
DT 28-JUL-2005 (first entry)
XX
DE Amino acid sequence of CD20 antigen binding molecule #6..
XX
KW antigen binding molecule; Fc receptor; B-cell marker; CD20;
KW antibody engineering; B-cell depletion; B cell lymphoma; cytostatic;
KW hematological disease; immune disorder; neoplasm.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN WO200504859-A2.
XX
PD 19-MAY-2005.
XX
PF 05-NOV-2004; 2004WO-IB003896.
XX
PR 05-NOV-2003; 2003US-0517096P.
XX
PA (GLYC-). GLYCART BIOTECHNOLOGY AG.
PA (UMAN/) UMANA P.
PA (BRUE/) BRUENKER P.
PA (FERR/) FERRARA C.
PA (SUTE/) SUTER T.
PA (PUEN/) PUENTENER U.
PA (MOES/) MOESSNER E.
XX
PI Umana P, Bruenker P, Ferrara C, Suter T, Puentener U, Moessner E;
XX WPI; 2005-347056/35.
DR N-PSDB; AEA18666.
XX
PT New polynucleotides and encoded antigen binding molecules with increased
PT Fc receptor binding affinity and effector function, useful for
PT diagnosing, preventing or treating B-cell proliferative disorders,
PT including B cell lymphoma.
XX
PS Claim 128; SEQ ID NO 40; 187pp; English.
XX

CC The specification describes antigen binding molecules with increased Fc
CC receptor binding affinity and effector function. These antigen binding
CC molecules may have modified glycosylation, and are especially specific
CC for human B-cell marker CD20. The invention is useful for diagnosing,
CC preventing or treating disorders or diseases treatable by B-cell
CC depletion, such as B cell lymphoma. The present sequence represents an
CC antigen binding molecule of the invention.
XX
SQ Sequence 119 AA;
Query Match 61.1%; Score 44; DB 9; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GYWLTIWG 9
Db 103 GYWLVIWG 110
Search completed: May 2, 2006, 08:54:58
Job time : 114.791 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 18.1395 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	2 S76385	hypothetical prote
2	45	62.5	828	2 AD0412	ATP-dependent heli
3	43.5	60.4	1993	2 T30902	sodium channel SCA
4	42.5	59.0	1765	2 T42388	sodium channel alp
5	42	58.3	72	2 S30980	gene 35 protein -
6	42	58.3	441	2 C95307	probable transport
7	42	58.3	1502	2 T42216	multidrug resistan
8	41.5	57.6	620	2 F70439	oxaloacetate decar
9	41	56.9	307	2 T48166	hypothetical prote
10	41	56.9	391	2 PC4117	replication protei
11	41	56.9	419	2 E90446	permease [imported
12	41	56.9	739	2 T29407	hypothetical prote
13	40.5	56.2	200	2 I48108	sodium channel alp
14	40.5	56.2	1681	2 A55138	sodium channel mNa
15	40.5	56.2	1682	2 A45380	sodium channel pro
16	40.5	56.2	1820	1 CHEE	sodium channel pro
17	40.5	56.2	1835	2 I54323	sodium channel alp
18	40.5	56.2	1836	2 I64893	sodium channel alp
19	40.5	56.2	1836	2 JS0648	sodium channel alp
20	40.5	56.2	1836	2 I51964	sodium channel alp
21	40.5	56.2	1840	1 CHRTM1	sodium channel pro
22	40.5	56.2	1951	2 S00320	sodium channel pro
23	40.5	56.2	1976	2 I56555	sodium channel pro
24	40.5	56.2	1977	2 S54771	sodium channel alp
25	40.5	56.2	1983	2 A60054	sodium channel pro
26	40.5	56.2	2005	2 A46269	sodium channel alp
27	40.5	56.2	2005	2 B25019	sodium channel pro
28	40.5	56.2	2009	2 A25019	sodium channel pro
29	40.5	56.2	2016	2 A38195	sodium channel pro

30	40.5	56.2	2019	2 A33996	sodium channel pro
31	40.5	56.2	2049	2 T43161	sodium channel pro
32	40	55.6	142	2 C34903	Ig heavy chain pre
33	40	55.6	339	2 F97190	phenylalanyl-tRNA
34	40	55.6	359	2 F95406	probable ABC trans
35	40	55.6	425	2 B71038	probable Na+/H+-ex
36	40	55.6	508	2 C95282	probable ABC trans
37	40	55.6	2344	2 S64740	genome polyprotein
38	39.5	54.9	298	2 AH0289	probable aldo/keto
39	39.5	54.9	345	1 JH0185	D-amino-acid oxida
40	39.5	54.9	347	1 OXPGDA	D-amino-acid oxida
41	39.5	54.9	347	1 S01340	D-amino-acid oxida
42	39.5	54.9	347	1 JX0132	D-amino-acid oxida
43	39	54.2	376	2 AF1978	hypothetical prote
44	39	54.2	392	2 A53580	neurexin III beta
45	39	54.2	426	2 B53580	neurexin III beta

ALIGNMENTS

RESULT 1

S76385
hypothetical protein - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yasu
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocyst*
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KAN>
A;Cross-references: UNIPROT:Q55705; UNIPARC:UPI00001394C5; EMBL:D64000; GB:AB001339; N
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable alkaline phosphatase yngC

Query Match 63.9%; Score 46; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9
|||: ||
Db 73 CGYWVGRWG 81

RESULT 2

AD0412
ATP-dependent helicase [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0412
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0412
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-828 <KUR>
A;Cross-references: UNIPROT:Q8ZBL4; UNIPARC:UPI00000CDA15; GB:AL590842; PIDN:CAC92624.
C;Genetics:
A;Gene: hrpB
C;Superfamily: ATP-dependent RNA helicase, HrpB type

Query Match 62.5%; Score 45; DB 2; Length 828;

Best Local Similarity 58.3%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10
||| : |||
Db 372 CGLWLELLSWGC 383

RESULT 3
T30902
sodium channel SCAP1 alpha chain - California sea hare
C:Species: Aplysia californica (California sea hare)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30902
R:Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A:Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A:Reference number: Z20929; MUID:97238630; PMID:9115644
A:Accession: T30902
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-1993 <DYE>
A:Cross-references: UNIPROT:P90670; UNIPARC:UPI000007A0B4; EMBL:U66915; NID:gl842248; PII
C:Superfamily: sodium channel protein

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
||| : |||
Db 942 CGEWIESMWGC 952

RESULT 4
T42388
sodium channel alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42388
R:Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A:Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periph
A:Reference number: Z22149; MUID:98338024; PMID:9671787
A:Accession: T42388
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-1765 <DIB>
A:Cross-references: UNIPROT:O88457; UNIPARC:UPI00000E8ABD; EMBL:AF059030; NID:g3372614;
A:Experimental source: strain Sprague-Dawley; dorsal root ganglia
A:Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
C:Superfamily: sodium channel protein

Query Match 59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
||| : |||
Db 754 CGEWIENMWGC 764

RESULT 5
S30980
gene 35 protein - Mycobacterium phage L5
C:Species: Mycobacterium phage L5
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30980
R:Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A:Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A:Reference number: S30949; MUID:93211283; PMID:8459767
A:Accession: S30980

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-72 <DON>
A:Cross-references: UNIPROT:Q05245; UNIPARC:UPI0000138557; EMBL:Z18946; NID:gl5859; PII
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Gene: 35

Query Match 58.3%; Score 42; DB 2; Length 72;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8
||| : |||
Db 50 CGMWLPVW 57

RESULT 6
C95307
probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) m
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004
C:Accession: C95307
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bo
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melil
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95307
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <KUR>
A:Cross-references: UNIPROT:Q92ZT6; UNIPARC:UPI00000CB08F; GB:AE006469; PIDN:AAK65021
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauro
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0684
A:Genome: plasmid
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 58.3%; Score 42; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
||| : |||
Db 92 GYWISIW 98

RESULT 7
T42216
multidrug resistance-associated protein homolog MLP-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42216
R:Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A:Title: Hepatic expression of multidrug resistance-associated protein-like proteins m
A:Reference number: Z22081; MUID:98279126; PMID:9614210
A:Accession: T42216
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-1502 <HIR>
A:Cross-references: UNIPROT:O88269; UNIPARC:UPI000012F57A; EMBL:AB010466; NID:g3242457
A:Experimental source: strain Sprague-Dawley; liver

C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 58.3%; Score 42; DB 2; Length 1502;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
Db 964 GYWLTLW 970

RESULT 8
F70439
oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70439
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.

Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70439
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-620 <AQF>
A;Cross-references: UNIPROT:O67544; UNIPARC:UPI000005667F; GB:AE000747; NID:G2983944; PI
A;Experimental source: strain VPS
C;Genetics:

C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bio
F;540-613/Domain: lipoyl/biotin-binding homology <LPB>
F;579/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 57.6%; Score 41.5; DB 2; Length 620;
Best Local Similarity 60.0%; Pred. No. 94;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYW-LTIWG 9
Db 38 CGFWSLEVWG 47

RESULT 9
T48166
hypothetical protein T1008.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48166
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24486
A;Accession: T48166
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <BEV>
A;Cross-references: UNIPROT:Q9M030; UNIPARC:UPI000009E479; EMBL:AL161746
A;Experimental source: cultivar Columbia; BAC clone T1008
C;Genetics:

A;Map position: 5
A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
A;Note: T1008.150

Query Match 56.9%; Score 41; DB 2; Length 307;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
Db 186 CSFVVSIGWC 195

RESULT 10

PC4117
replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A;Reference number: JC4514; MUID:96105215; PMID:8529878
A;Accession: PC4117
A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: UNIPARC:UPI000017AEAF; DDBJ:D50018

Query Match 56.9%; Score 41; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIWG 9
Db 155 YWLTEWG 161

RESULT 11
E90446
permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Cross-references: UNIPROT:Q97VB7; UNIPARC:UPI000006481C; GB:AE006641; NID:G13816037;
C;Genetics:
A;Gene: SSO2718

Query Match 56.9%; Score 41; DB 2; Length 419;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
Db 365 GFWEITLWG 372

RESULT 12
T29407
hypothetical protein C16C8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T29407
R;Waterston, R.; Le, T.T.; Gattung, S.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C16C8.
A;Reference number: Z20617
A;Accession: T29407
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-739 <WAT>
A;Cross-references: UNIPARC:UPI0000175207; EMBL:U80452; PIDN:AAB37863.1; GSPDB:GN00002C
A;Experimental source: strain Bristol N2; clone C16C8
C;Genetics:
A;Gene: CESP:C16C8.2
A;Map position: 2
A;Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2;

C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 56.9%; Score 41; DB 2; Length 739;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
|||:|:|
Db 118 CGFWATIREC 127

RESULT 13

I48108
sodium channel alpha subunit - long-tailed hamster (fragment)
C;Species: Cricetus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48108
R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A;Reference number: I48107
A;Accession: I48108
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-200 <RES>
A;Cross-references: UNIPROT:Q60464; UNIPARC:UPI00000E60A9; GB:M87541; NID:g191069; PIDN:
C;Genetics:
A;Gene: chol
C;Superfamily: sodium channel protein
C;Keywords: duplication

Query Match 56.2%; Score 40.5; DB 2; Length 200;
Best Local Similarity 54.5%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||:|:|
Db 26 CGEWETLWDC 36

RESULT 14

A55138
sodium channel mNa2.3, voltage-gated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A55138
R;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.
J. Biol. Chem. 269, 30125-30131, 1994
A;Title: Primary structure and differential expression during development and pregnancy
A;Reference number: A55138; MUID:95074002; PMID:7982916
A;Accession: A55138
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1681 <FEL>
A;Cross-references: UNIPROT:Q62467; UNIPARC:UPI0000049623; GB:L36179; NID:g609544; PIDN:
C;Superfamily: sodium channel protein

Query Match 56.2%; Score 40.5; DB 2; Length 1681;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||:|:|
Db 686 CGEWETLWEC 696

RESULT 15

A45380
sodium channel protein alpha chain hNav2.1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45380
R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992
A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in hu
A;Reference number: A45380; MUID:92279233; PMID:1317577
A;Accession: A45380
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1682 <GEO>
A;Cross-references: UNIPROT:Q01118; UNIPARC:UPI00001279D2; GB:M91556; NID:g189046; PID:
A;Experimental source: heart
A;Note: sequence extracted from NCBI backbone (NCBIP:104344)
C;Superfamily: sodium channel protein
C;Keywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-ga

Query Match 56.2%; Score 40.5; DB 2; Length 1682;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||:|:|
Db 686 CGEWETLWDC 696

Search completed: May 2, 2006, 08:56:21
Job time : 19.1395 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 113.256 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	63.9	218	Y232_S3YN3	Q55705 synechocyst
2	45.5	63.2	173	Q4Y1C8_PLACH	Q4Y1C8 plasmodium
3	45	62.5	360	Q67Q12_SYMTH	Q67Q12 symbiobacte
4	45	62.5	828	Q8ZBL4_YERPE	Q8ZBL4 yersinia pe
5	45	62.5	828	Q66EF6_YERPE	Q66EF6 yersinia pe
6	45	62.5	853	Q8D1A7_YERPE	Q8D1A7 yersinia pe
7	43.5	60.4	1993	P90670_APLCA	P90670 aplysia cal
8	43	59.7	168	Q6H022_FREDI	Q6H022 fremyella d
9	43	59.7	215	Q57Z63_9TRYP	Q57Z63 trypanosoma
10	43	59.7	220	Q4QID2_LEIMA	Q4QID2 leishmania
11	43	59.7	221	Q74JK6_LACJO	Q74JK6 lactobacill
12	43	59.7	454	Q59NK9_CANAL	Q59NK9 candida alb
13	43	59.7	501	Q6C574_YARLI	Q6C574 yarrowia li
14	43	59.7	520	Q4XP68_PLACH	Q4XP68 plasmodium
15	43	59.7	646	Q8DKD6_SYNEL	Q8DKD6 synechococ
16	43	59.7	733	Q8H2N7_ORYSA	Q8H2N7 oryza sativ
17	43	59.7	1084	Q7WY20_PSEAE	Q7WY20 pseudomonas
18	42.5	59.0	152	1 ATRAP_PONPY	Q5rer2 pongo pygma
19	42.5	59.0	159	1 ATRAP_HUMAN	Q6rw13 homo sapien
20	42.5	59.0	263	2 Q7YVF1_CRYPV	Q7YVF1 cryptospori
21	42.5	59.0	263	2 Q5CNC4_CRYHO	Q5cnc4 cryptospori
22	42.5	59.0	1765	1 SC11A_RAT	Q88457 rattus norv
23	42	58.3	72	1 VG35_BPMLS	Q05245 mycobacteri
24	42	58.3	133	2 Q855L3_9CAUD	Q855L3 mycobacteri
25	42	58.3	284	2 Q6MC01_PARUW	Q6mc01 parachlamyd
26	42	58.3	314	2 Q4NT43_9DELT	Q4nt43 anaeromyxob
27	42	58.3	343	2 Q94FS2_CAJCA	Q94fs2 cajanus caj
28	42	58.3	389	2 Q83I51_TROW8	Q83i51 tropheryma
29	42	58.3	441	2 Q92ZT6_RHIME	Q92zt6 rhizobium m
30	42	58.3	452	2 Q83G14_TROWT	Q83g14 tropheryma
31	42	58.3	472	1 RBL_NITVU	Q59613 nitrobacter

32	42	58.3	473	2	Q8VQ84_9PROT	Q8vq84 nitrosospir
33	42	58.3	473	2	Q9XD76_NITWI	Q9xd76 nitrobacter
34	42	58.3	473	2	Q9XD77_NITWI	Q9xd77 nitrobacter
35	42	58.3	1308	2	Q8T6H2_DICDI	Q8t6h2 dictyosteli
36	42	58.3	1328	2	Q54EK2_DICDI	Q54ek2 dictyosteli
37	42	58.3	1498	1	MRP6_MOUSE	Q9rls7 mus musculu
38	42	58.3	1502	1	MRP6_RAT	O88269 rattus norv
39	42	58.3	1503	1	MRP6_HUMAN	O95255 homo sapien
40	41.5	57.6	122	2	Q8N1Z5_HUMAN	O8n1z5 homo sapien
41	41.5	57.6	473	2	Q5T2N8_HUMAN	O5t2n8 homo sapien
42	41.5	57.6	620	2	O67544_AQUAE	O67544 aquifex aeo
43	41	56.9	266	2	Q82Z85_ENTFA	Q82z85 enterococcu
44	41	56.9	307	2	Q9M030_ARATH	Q9m030 arabidopsis
45	41	56.9	376	1	ETRI_YARLI	Q6cbe4 yarrowia li

ALIGNMENTS

RESULT 1
Y232_S3YN3
ID Y232_S3YN3 STANDARD; PRT; 218 AA.
AC Q55705;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein slr0232.
GN OrderedLocusNames=slr0232;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the deda family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; BA000022; BAA10237.1; -; Genomic_DNA.
DR PIR; S76385; S76385.
DR InterPro; IPR000252; Deda.
DR Pfam; PF00597; Deda; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 218 AA; 23782 MW; C04B5D7B7EA7F863 CRC64;

Query Match 63.9%; Score 46; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9

```
Db
|||||: ||
73 CGYVGRWG 81

RESULT 2
Q4Y1C8 PLACH PRELIMINARY; PRT; 173 AA.
AC Q4Y1C8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PC103204.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01001794; CAH77032.1; -; Genomic_DNA.
KW 'Hypothetical protein.
SQ SEQUENCE 173 AA; 21349 MW; 053E43204D83013F CRC64;

Query Match 63.2%; Score 45.5; DB 2; Length 173;
Best Local Similarity 72.7%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 CGYWL---TIW 8
|||: |||
Db 12 CGYWLFEKTIW 22

RESULT 3
Q67QI2 SYMTH
ID Q67QI2 SYMTH PRELIMINARY; PRT; 360 AA.
AC Q67QI2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=STH1076;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=T / IAM 14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD40061.1; -; Genomic_DNA.
DR GO; GO:0004222; F:metallopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR Pfam; PF01551; Peptidase_M23; I.
KW Complete proteome; Copper; Hypothetical protein; Metal-binding;
KW Oxidoreductase.

SQ SEQUENCE 360 AA; 39433 MW; EEE0B58F939CE443 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 360;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
|||: |||
Db 127 GYWLTIW 133

RESULT 4
Q8ZBL4 YERPE
ID Q8ZBL4 YERPE PRELIMINARY; PRT; 828 AA.
AC Q8ZBL4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ATP-dependent helicase.
GN Name=hrpB; OrderedLocusNames=YPO3394;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414156; CAC92624.1; -; Genomic_DNA.
DR PIR; AD0412; AD0412.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR010225; DEAH_box_HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMs; TIGR01970; DEAH_box_HrpB; 1.
DR ATP-binding; Complete proteome; Helicase; Hydrolase.
KW ATP-binding; Complete proteome; Helicase; Hydrolase.
SQ SEQUENCE 828 AA; 91983 MW; 3A11F88835D5E583 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 828;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC.10
|||: |||
Db 372 CGLWLELLSWGC 383

RESULT 5
Q66EF6 YERPS
ID Q66EF6 YERPS PRELIMINARY; PRT; 828 AA.
AC Q66EF6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
```

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Helicase, ATP-dependent.
GN Name=hrp; Synonyms=yadO; OrderedLocusNames=YPTB0737;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR010225; DEAD_box_HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMS; TIGR01970; DEAD_box_HrpB; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolyase.
SQ SEQUENCE 828 AA; 91983 MW; CF11FFDD863330635 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 828;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10
Db 372 CGLWLELLSWGC 383

RESULT 6
Q8DIA7 YERPE
ID Q8DIA7_YERPE PRELIMINARY; PRT; 853 AA.
AC Q8DIA7; Q74XU2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Helicase, ATP-dependent.
GN Name=hrpB; OrderedLocusNames=YP0291, Y0794;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM";
RL J. Bacteriol. 184:4601-4611(2002).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=91001;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans";
RL DNA Res. 11:179-197(2004).
DR EMBL; AE013681; AAM84381.1; -; Genomic_DNA.
DR EMBL; AE017128; AAS60566.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR010225; DEAD_box_HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMS; TIGR01970; DEAD_box_HrpB; 1.
KW ATP-binding; Helicase; Hydrolyase.
SQ SEQUENCE 853 AA; 95005 MW; B3DB738A18665B42 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 853;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10
Db 397 CGLWLELLSWGC 408

RESULT 7
P90670 APLCA
ID P90670_APLCA PRELIMINARY; PRT; 1993 AA.
AC P90670;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sodium channel alpha-subunit SCAP1.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nervous system;
RX MEDLINE=97238630; PubMed=9115644;
RA Dyer J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
RT "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
RT subunit cDNA";
RL DNA Cell Biol. 16:347-356(1997).
DR EMBL; U66915; AAC47457.1; -; mRNA.
DR PIR; T30902; T30902.
DR HSSP; P04775; 1BYV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.

```
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Sodium transport;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 1e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||: :|||
Db 942 CGEWIESMWGC 952

RESULT 8
Q6H022_FREDI PRELIMINARY; PRT; 168 AA.
AC Q6H022;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OX NCBI_TaxID=1197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FD33;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
RT Regulated by Light Color in the Cyanobacterium Fremyella
RT diplosiphon.";
RL J. Bacteriol. 186:4338-4349(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FD33;
RA Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548455; AAT41947.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 18932 MW; 1C9DB963D5210332 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 168;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWLTIWG 9
|||||: :|
Db 122 CGYWLSLRG 130

RESULT 9
Q57Z63_9TRYP PRELIMINARY; PRT; 215 AA.
AC Q57Z63;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Tb927.5.3300;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;

DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Sodium transport;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 215;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWGC 10
|: :|
Db 123 WYTLWGC 129

RESULT 10
Q4QID2_LEIMA PRELIMINARY; PRT; 220 AA.
AC Q4QID2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF08.0370;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005247; CAJ02216.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 220 AA; 26176 MW; 3AE510340D9F5583 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 220;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWGC 10
|: :|
Db 128 WYTLWGC 134

RESULT 11
Q74JK6_LACJO PRELIMINARY; PRT; 221 AA.
AC Q74JK6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN OrderedLocusNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
```


OX NCBI_TaxID=33959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019835; P:cytolysis; IEA.
DR InterPro; IPR004254; HlyIII-related.
DR InterPro; IPR005744; HlyIII.
DR Pfam; PF03006; HlyIII; 1.
DR TIGRFAMs; TIGR01065; hlyIII; 1.
KW Complete proteome.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|:|:|:|
Db 172 GFLLVWG 179

RESULT 12
Q59NK9 CANAL
ID Q59NK9 CANAL PRELIMINARY; PRT; 454 AA.
AC Q59NK9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CaO19.6606;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans."
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC00100204; EAK92073.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 454 AA; 51731 MW; A69ECDF7893B914D CRC64;

Query Match 59.7%; Score 43; DB 2; Length 454;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIWGC 10
||| | |

Db 137 YWLTGWSC 144

RESULT 13
Q6C574 YARLI
ID Q6C574 YARLI PRELIMINARY; PRT; 501 AA.
AC Q6C574;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome E of strain CLIB99 of Yarrowia
DE lipolytica.
GN OrderedLocusNames=YALI0E204719;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=1529592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
DR EMBL; CR382131; CAG79783.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;

Query Match 59.7%; Score 43; DB 2; Length 501;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 10
||:|:|:|
Db 157 GYLTLMYC 165

RESULT 14
Q4XP68 PLACH
ID Q4XP68 PLACH PRELIMINARY; PRT; 520 AA.
AC Q4XP68;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Pc-fam-2 protein, putative (Fragment).
GN ORFNames=PC108181.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01004254; CAH81294.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 520 AA; 52230 MW; 08E31B477FEFD368 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 520;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|||: ||
Db 167 GYWLSNWG 174

RESULT 15

Q8DKD6_SYNEL
ID Q8DKD6_SYNEL PRELIMINARY; PRT; 646 AA.
AC Q8DKD6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T110923 protein.
GN OrderedLocusNames=t110923;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneo T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; BA000039; BAC08475.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR01932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C_SIG; 1.
KW Complete proteome.
SQ SEQUENCE 646 AA; 71071 MW; 56C5A74F76652D56 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 646;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIWGC 10
||: |||
Db 415 YWINRWGC 422

Search completed: May 2, 2006, 08:46:50
Job time : 115.256 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 28.3721 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44.5	61.8	1024	2	US-09-562-737-84
2	43	59.7	492	2	US-09-107-532A-6945
3	42.5	59.0	1024	2	US-09-562-737-86
4	42.5	59.0	1765	2	US-09-354-147C-2
5	42.5	59.0	1765	2	US-09-354-147C-3
6	42	58.3	161	2	US-09-325-932A-187
7	42	58.3	273	2	US-09-270-767-46926
8	42	58.3	1498	2	US-09-792-616-9
9	42	58.3	1503	2	US-09-792-616-3
10	42	58.3	1503	2	US-09-647-140B-8
11	41	56.9	222	2	US-09-071-035-408
12	41	56.9	222	2	US-10-206-576-408
13	41	56.9	229	2	US-09-134-000C-3630
14	41	56.9	264	2	US-09-540-236-2978
15	41	56.9	266	2	US-09-071-035-406
16	41	56.9	266	2	US-10-206-576-406
17	40.5	56.2	1024	2	US-09-562-737-81
18	40.5	56.2	1024	2	US-09-562-737-87
19	40.5	56.2	1525	2	US-09-949-016-10988
20	40.5	56.2	1681	2	US-09-920-653B-3
21	40.5	56.2	1835	2	US-08-836-325-15
22	40.5	56.2	1835	2	US-09-457-571-15
23	40.5	56.2	1836	2	US-10-162-012-24
24	40.5	56.2	1969	2	US-08-836-325-16
25	40.5	56.2	1969	2	US-09-457-571-16
26	40.5	56.2	1976	2	US-09-024-020B-9
27	40.5	56.2	1976	2	US-09-425-043-9

28	40.5	56.2	1977	2	US-09-976-594-757	Sequence 757, App
29	40.5	56.2	1977	2	US-09-919-039-367	Sequence 367, App
30	40.5	56.2	1978	2	US-09-024-020B-3	Sequence 3, Appli
31	40.5	56.2	1978	2	US-09-425-043-3	Sequence 3, Appli
32	40.5	56.2	1984	2	US-08-836-325-10	Sequence 10, Appl
33	40.5	56.2	1984	2	US-09-457-571-10	Sequence 10, Appl
34	40.5	56.2	1988	2	US-09-024-020B-4	Sequence 4, Appli
35	40.5	56.2	1988	2	US-09-425-043-4	Sequence 4, Appli
36	40.5	56.2	1989	2	US-08-836-325-11	Sequence 11, Appl
37	40.5	56.2	1989	2	US-08-836-325-12	Sequence 12, Appl
38	40.5	56.2	1989	2	US-09-457-571-11	Sequence 11, Appl
39	40.5	56.2	1989	2	US-09-457-571-12	Sequence 12, Appl
40	40.5	56.2	1989	2	US-09-949-016-10076	Sequence 10076, A
41	40.5	56.2	2005	2	US-08-836-325-7	Sequence 7, Appli
42	40.5	56.2	2005	2	US-09-457-571-7	Sequence 7, Appli
43	40.5	56.2	2016	2	US-09-634-920-4	Sequence 4, Appli
44	40.5	56.2	2016	2	US-09-514-907A-2	Sequence 2, Appli
45	40.5	56.2	2016	2	US-09-896-994-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-562-737-84
; Sequence 84, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-84

Query Match 61.8%; Score 44.5; DB 2; Length 1024;
Best Local Similarity 54.5%; Pred. No. 2e+02; 1; Indels 1; Gaps 1;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 1 CGYWL-TIWGC 10
||:|:|:|
Db 892 CGHWIETMWDC 902

RESULT 2
US-09-107-532A-6945
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM: CD/ROM ISO9660
; MEDIUM TYPE: PC
; COMPUTER: PC

OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B).LOCATION 1....492
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945

Query Match 59.7%; Score 43; DB 2; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
|||
Db 112 GYWLTCW 118

RESULT 3
US-09-562-737-86
Sequence 86, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 1024
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
US-09-562-737-86

Query Match 59.0%; Score 42.5; DB 2; Length 1024;
Best Local Similarity 63.6%; Pred. No. 3.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||
Db 892 CGEWLETMWDC 902

RESULT 4

US-09-354-147C-2.
Sequence 2, Application US/09354147C
Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1765
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: UNSURE
LOCATION: (652) ..(1334)
OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn
OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.
US-09-354-147C-2

Query Match 59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||
Db 754 CGEWIENMWGC 764

RESULT 5
US-09-354-147C-3
Sequence 3, Application US/09354147C
Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1765
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: putative amino acid seq. of rat NaN
US-09-354-147C-3

Query Match 59.0%; Score 42.5; DB 2; Length 1765;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||
Db 754 CGEWIENMWGC 764


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RESULT 6
US-09-325-932A-187
; Sequence 187, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-187

Query Match      58.3%; Score 42; DB 2; Length 161;
Best Local Similarity 56.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWGC 10
      |||||: ||
Db      100 GYWLNLSCG 108

RESULT 7
US-09-270-767-46926
; Sequence 46926, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 46926
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46926

Query Match      58.3%; Score 42; DB 2; Length 273;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWLTIW 8
      |||||: ||
Db      266 CGYWATIF 273

RESULT 8
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498

US-09-325-932A-187
; Sequence 187, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-187

Query Match      58.3%; Score 42; DB 2; Length 161;
Best Local Similarity 56.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWGC 10
      |||||: ||
Db      100 GYWLNLSCG 108

RESULT 7
US-09-270-767-46926
; Sequence 46926, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 46926
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46926

Query Match      58.3%; Score 42; DB 2; Length 273;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWLTIW 8
      |||||: ||
Db      266 CGYWATIF 273

RESULT 8
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      58.3%; Score 42; DB 2; Length 1498;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||||: ||
Db      960 GYWLTLW 966

RESULT 9
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      58.3%; Score 42; DB 2; Length 1503;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||||: ||
Db      965 GYWLTLW 971

RESULT 10
US-09-647-140B-8
; Sequence 8, Application US/09647140B
; Patent No. 6803184
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun.
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US99/06644
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-647-140B-8

Query Match      58.3%; Score 42; DB 2; Length 1503;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
| | | | | : |
Db 965 GYWLSLW 971

RESULT 11
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brooks
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-408

Query Match 56.9%; Score 41; DB 2; Length 222;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
| | | | | : |
Db 179 GTWITLWG 186

RESULT 12
US-10-206-576-408
; Sequence 408, Application US/10206576
; Patent No. 6913907
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 408:
US-10-206-576-408

Query Match 56.9%; Score 41; DB 2; Length 222;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
| | | | | : |
Db 179 GTWITLWG 186

RESULT 13
US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3630
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630

Query Match 56.9%; Score 41; DB 2; Length 229;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
| | | | | : |
Db 203 GTWITLWG 210

RESULT 14

US-09-540-236-2978
; Sequence 2978, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2978
; LENGTH: 264
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2978

Query Match 56.9%; Score 41; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. NO. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWLTIW 8
||| |||
Db 200 CGAWLGIW 207

RESULT 15
US-09-071-035-406
; Sequence 406, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-406

Query Match 56.9%; Score 41; DB 2; Length 266;
Best Local Similarity 62.5%; Pred. NO. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9
|||:|
Db 203 GTWITLWG 210

Search completed: May 2, 2006, 08:58:27
Job time : 29.3721 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 93.0233 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	72	100.0	10	4	US-10-046-922-35
2	54	75.0	10	4	US-10-046-922-34
3	50	69.4	10	4	US-10-046-922-73
4	47.5	66.0	304	4	US-10-017-161-2288
5	47.5	66.0	304	4	US-10-292-798-1934
6	47	65.3	25	4	US-10-280-066-476
7	47	65.3	63	4	US-10-437-963-125253
8	46	63.9	17	4	US-10-125-869A-54
9	46	63.9	17	4	US-10-462-262-278
10	46	63.9	136	4	US-10-112-944-743
11	45	62.5	828	4	US-10-282-122A-77862
12	44.5	61.8	1024	4	US-10-211-962-84
13	44	61.1	103	4	US-10-437-963-181150
14	44	61.1	112	5	US-10-981-738-1
15	44	61.1	119	5	US-10-981-738-30
16	44	61.1	119	5	US-10-981-738-32
17	44	61.1	119	5	US-10-981-738-34
18	44	61.1	119	5	US-10-981-738-36
19	44	61.1	119	5	US-10-981-738-38
20	44	61.1	119	5	US-10-981-738-40
21	44	61.1	119	5	US-10-981-738-42
22	44	61.1	119	5	US-10-981-738-44
23	44	61.1	119	5	US-10-981-738-46
24	44	61.1	119	5	US-10-981-738-48
25	44	61.1	119	5	US-10-981-738-50
26	44	61.1	119	5	US-10-981-738-52
27	44	61.1	119	5	US-10-981-738-54

28	44	61.1	119	5	US-10-981-738-56	Sequence 56, Appl
29	44	61.1	119	5	US-10-981-738-58	Sequence 58, Appl
30	44	61.1	119	5	US-10-981-738-60	Sequence 60, Appl
31	44	61.1	119	5	US-10-981-738-62	Sequence 62, Appl
32	44	61.1	119	5	US-10-981-738-64	Sequence 64, Appl
33	44	61.1	119	5	US-10-981-738-66	Sequence 66, Appl
34	44	61.1	119	5	US-10-981-738-68	Sequence 68, Appl
35	44	61.1	119	5	US-10-981-738-70	Sequence 70, Appl
36	44	61.1	119	5	US-10-981-738-72	Sequence 72, Appl
37	44	61.1	161	4	US-10-767-701-54778	Sequence 54778, A
38	44	61.1	468	5	US-10-981-738-13	Sequence 13, Appl
39	43	59.7	13	4	US-10-125-869A-73	Sequence 73, Appl
40	43	59.7	13	4	US-10-462-262-297	Sequence 297, App
41	43	59.7	291	4	US-10-369-493-19313	Sequence 19313, A
42	43	59.7	454	4	US-10-032-585-7816	Sequence 7816, Ap
43	43	59.7	459	4	US-10-437-963-160191	Sequence 160191,
44	43	59.7	474	4	US-10-282-122A-57928	Sequence 57928, A
45	43	59.7	671	4	US-10-437-963-190740	Sequence 190740,

ALIGNMENTS

RESULT 1
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; US-10-046-922-35

Query Match 100.0%; Score 72; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
Db 1 CGYWLTIWGC 10

RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)

; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 75.0%; Score 54; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|||
Db 2 GYWLTIWG 9

RESULT 3
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73

Query Match 69.4%; Score 50; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 1 CGYWLTIWGC 10
|||
Db 1 CGYWXWXC 10

RESULT 4
US-10-017-161-2288
; Sequence 2288, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2288
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: MOD_RES
; LOCATION: (73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (79)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (85)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (123)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (162)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (194)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (219)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288

Query Match 66.0%; Score 47.5; DB 4; Length 304;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10
|||
Db 108 CGFW-AWGC 116

```
RESULT 5
US-10-292-798-1934
; Sequence 1934, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1934
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (73)..(73)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (80)..(83)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (89)..(91)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (96)..(97)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (101)..(101)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (107)..(107)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (118)..(119)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (121)..(121)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (123)..(123)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (178)..(178)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (210)..(211)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (219)..(219)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
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; NAME/KEY: MOD_RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-292-798-1934
Query Match 66.0%; Score 47.5; DB 4; Length 304;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 CGYWLTIWGC 10
Db 108 CGFW-AVWGC 116
RESULT 6
US-10-280-066-476
; Sequence 476, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BI
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 476
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Tiel-20C-3-D116
US-10-280-066-476
Query Match 65.3%; Score 47; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGYWLTIWGC 9
Db 5 CGYWGELWG 13
RESULT 7
US-10-437-963-125253
; Sequence 125253, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125253
; LENGTH: 63
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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.1.pep
US-10-437-963-125253

Query Match      65.3%; Score 47; DB 4; Length 63;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
Db      37 CGHYLKAWGC 46

RESULT 8
US-10-125-869A-54
; Sequence 54, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-54

Query Match      63.9%; Score 46; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 9
Db      4 CGFWPRIWG 12

RESULT 9
US-10-462-262-278
; Sequence 278, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide

```

```

US-10-462-262-278

Query Match      63.9%; Score 46; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 9
Db      4 CGFWPRIWG 12

RESULT 10
US-10-112-944-743
; Sequence 743, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 743
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(136)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set f
; OTHER INFORMATION: in Example 2
US-10-112-944-743

Query Match      63.9%; Score 46; DB 4; Length 136;
Best Local Similarity 60.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
Db      93 CGRWDWLWGC 102

RESULT 11
US-10-282-122A-77862

```

```

/ GENERAL INFORMATION:
/
/ APPLICANT: Umana, Pablo
/
/ APPLICANT: Bruenker, Peter
/
/ APPLICANT: Suter, Tobias
/
/ APPLICANT: Puentener, Ursula
/
/ APPLICANT: Moessner, Ekkehard
/
/ APPLICANT: Ferrara, Claudia
/
/ TITLE OF INVENTION: Antigen Binding Molecules
/
/ TITLE OF INVENTION: Affinity and Effectors
/
/ FILE REFERENCE: 1975.0290001
/
/ CURRENT APPLICATION NUMBER: US/10/981,738
/
/ CURRENT FILING DATE: 2004-11-05
/
/ NUMBER OF SEQ ID NOS: 78
/
/ SOFTWARE: Patentin version 3.3
/
/ SEQ ID NO 1
/
/ LENGTH: 112

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; TYPE: PRT
; ORGANISM: Mus sp.
US-10-981-738-1
Query Match      61.1%; Score 44; DB 5; Length 112;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GYWLTIWG 9
      |||||
Db      96 GYWLVIWG 103

RESULT 15
US-10-981-738-30
; Sequence 30, Application US/10981738
; Publication No. US20050123546A1
; GENERAL INFORMATION:
; APPLICANT: Umana, Pablo
; APPLICANT: Bruenker, Peter
; APPLICANT: Suter, Tobias
; APPLICANT: Puenteener, Ursula
; APPLICANT: Moessner, Ekkehard
; APPLICANT: Ferrara, Claudia
; TITLE OF INVENTION: Antigen Binding Molecules with Increased Fc Receptor Binding
; TITLE OF INVENTION: Affinity and Effector Function
; FILE REFERENCE: 1975.0290001
; CURRENT APPLICATION NUMBER: US/10/981,738
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mouse-human chimeric polypeptide
US-10-981-738-30
Query Match      61.1%; Score 44; DB 5; Length 119;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GYWLTIWG 9
      |||||
Db      103 GYWLVIWG 110

Search completed: May 2, 2006, 09:32:40
Job time : 94.0233 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw_model

Run on: May 2, 2006, 09:26:17 ; Search time 14.186 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 232119 seqs, 45477862 residues
Total number of hits satisfying chosen parameters: 232119
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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4: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42.5	59.0	152	11 US-11-264-096-1533	Sequence 1533, Ap
2	42.5	59.0	159	11 US-11-264-096-1534	Sequence 1534, Ap
3	42	58.3	441	11 US-11-087-099-2305	Sequence 2305, Ap
4	42	58.3	1023	9 US-10-995-561-968	Sequence 968, App
5	41	56.9	395	11 US-11-124-367A-322	Sequence 322, App
6	41	56.9	432	11 US-11-124-367A-326	Sequence 326, App
7	41	56.9	637	11 US-11-124-367A-321	Sequence 321, App
8	40.5	56.2	268	11 US-11-096-568A-19834	Sequence 19834, A
9	40.5	56.2	1981	9 US-10-374-954-23	Sequence 23, Appl
10	40.5	56.2	1998	9 US-10-374-954-21	Sequence 21, Appl
11	40.5	56.2	2009	9 US-10-374-954-2	Sequence 2, Appli
12	40	55.6	10	11 US-11-129-741-3641	Sequence 3641, Ap
13	40	55.6	119	11 US-11-250-411-97	Sequence 97, Appl
14	40	55.6	119	11 US-11-250-411-101	Sequence 101, Appl
15	40	55.6	138	11 US-11-250-411-86	Sequence 86, Appl
16	40	55.6	138	11 US-11-250-411-90	Sequence 90, Appl
17	40	55.6	167	11 US-11-236-198-33	Sequence 33, Appl
18	39.5	54.9	174	11 US-11-188-298-2376	Sequence 2376, Ap
19	39	54.2	257	11 US-11-087-099-983	Sequence 983, App
20	39	54.2	318	11 US-11-087-099-6672	Sequence 6672, Ap
21	39	54.2	342	11 US-11-087-099-2365	Sequence 2365, Ap

22	39	54.2	401	11 US-11-096-568A-25197	Sequence 25197, A
23	39	54.2	419	11 US-11-096-568A-25196	Sequence 25196, A
24	39	54.2	433	11 US-11-087-099-567	Sequence 567, App
25	39	54.2	450	11 US-11-096-568A-25195	Sequence 25195, A
26	39	54.2	454	11 US-11-087-099-4113	Sequence 4113, Ap
27	39	54.2	471	11 US-11-188-298-19864	Sequence 19864, A
28	39	54.2	475	11 US-11-188-298-6764	Sequence 6764, Ap
29	39	54.2	476	11 US-11-087-099-1256	Sequence 1256, Ap
30	39	54.2	478	11 US-11-087-099-7019	Sequence 7019, Ap
31	39	54.2	478	11 US-11-087-099-9555	Sequence 9555, Ap
32	39	54.2	478	11 US-11-188-298-8872	Sequence 8872, Ap
33	38.5	53.5	18	11 US-11-106-415-217	Sequence 217, App
34	38.5	53.5	18	11 US-11-233-256-217	Sequence 217, App
35	38.5	53.5	458	11 US-11-087-099-5844	Sequence 5844, Ap
36	38	52.8	253	11 US-11-096-568A-7538	Sequence 7538, Ap
37	38	52.8	322	11 US-11-087-099-2014	Sequence 2014, Ap
38	38	52.8	349	11 US-11-188-298-17452	Sequence 17452, A
39	38	52.8	363	9 US-10-444-926-10	Sequence 10, Appl
40	38	52.8	382	9 US-10-444-926-8	Sequence 8, Appli
41	38	52.8	387	9 US-10-444-926-14	Sequence 14, Appl
42	38	52.8	389	11 US-11-096-568A-8051	Sequence 8051, Ap
43	38	52.8	391	11 US-11-127-877-52	Sequence 52, Appl
44	38	52.8	400	11 US-11-096-568A-7537	Sequence 7537, Ap
45	38	52.8	415	9 US-10-444-926-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-11-264-096-1533
; Sequence 1533, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1533
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1533

Query Match 59.0%; Score 42.5; DB 11; Length 152;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYW-LTIWGC 10
|:| |||||
Db 14 GHWLLTTWGC 23

RESULT 2
US-11-264-096-1534
; Sequence 1534, Application US/11264096
; Publication No. US20060084794A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096

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; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1534
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1534

Query Match      59.0%; Score 42.5; DB 11; Length 159;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      2 GYW-LTIWGC 10
      |:| ||| |||
Db      14 GHWLLTTWGC 23

RESULT 3
US-11-087-099-2305
; Sequence 2305, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2305
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-11-087-099-2305

Query Match      58.3%; Score 42; DB 11; Length 441;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||::|
Db      92 GYWISIW 98

RESULT 4
US-10-995-561-968
; Sequence 968, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 968
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-968

Query Match      58.3%; Score 42; DB 9; Length 1023;
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```
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||::|
Db      485 GYWLSLW 491

RESULT 5
US-11-124-367A-322
; Sequence 322, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-322

Query Match      56.9%; Score 41; DB 11; Length 395;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 GYWLTIWGC 10
      ||| |||
Db      20 GIWFLFWGC 28

RESULT 6
US-11-124-367A-326
; Sequence 326, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-326

Query Match      56.9%; Score 41; DB 11; Length 432;
Best Local Similarity 55.6%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 2 GYWLTIWGC 10
| | | | |
Db 20 GIWFLFWGC 28

RESULT 7

US-11-124-367A-321
; Sequence 321, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-321

Query Match 56.9%; Score 41; DB 11; Length 637;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GYWLTIWGC 10
| | | | |
Db 20 GIWFLFWGC 28

RESULT 8

US-11-096-568A-19834
; Sequence 19834, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19834
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(268)
; OTHER INFORMATION: Ceres Seq. ID no. 12374913
US-11-096-568A-19834

Query Match 56.2%; Score 40.5; DB 11; Length 268;
Best Local Similarity 54.5%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 CGYW-LTIWGC 10
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Db 189 CGVWGALLWGC 199

RESULT 9

US-10-374-954-23

; Sequence 23, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-23

Query Match 56.2%; Score 40.5; DB 9; Length 1981;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
| | | | |
Db 921 CGEWIETMWDC 931

RESULT 10

US-10-374-954-21
; Sequence 21, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-21

Query Match 56.2%; Score 40.5; DB 9; Length 1998;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
| | | | |
Db 938 CGEWIETMWDC 948

RESULT 11

US-10-374-954-2
; Sequence 2, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2

; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2009
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-954-2

Query Match 56.2%; Score 40.5; DB 9; Length 2009;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
|||:|:|
Db 949 CGEWETMWDG 959

RESULT 12
US-11-129-741-3641
; Sequence 3641, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3641
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-3641

Query Match 55.6%; Score 40; DB 11; Length 10;
Best Local Similarity 71.4%; Pred. No. 8;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
|||:|
Db 2 GYWLCLW 8

RESULT 13
US-11-250-411-97
; Sequence 97, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718

; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 55.6%; Score 40; DB 11; Length 119;
Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|||:|
Db 103 GYWFAYWG 110

RESULT 14
US-11-250-411-101
; Sequence 101, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-101

Query Match 55.6%; Score 40; DB 11; Length 119;
Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
|||:|
Db 103 GYWFAYWG 110

RESULT 15
US-11-250-411-86
; Sequence 86, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA
APPLICANT: ITO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
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PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 138
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-86

Query Match 55.6%; Score 40; DB 11; Length 138;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTING 9
Db 122 GYWFAYWG 129

Search completed: May 2, 2006, 09:33:44
Job time : 14.186 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 78.9535 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	10	AAB99759	Aab99759 Rhesus D
2	34	97.1	12	AAB99769	Aab99769 Rhesus D
3	34	97.1	452	AAU03644	Aau03644 Group B S
4	34	97.1	466	ABU21589	Abu21589 Protein e
5	34	97.1	469	ADS44861	Ads44861 Bacterial
6	34	97.1	472	ABU38334	Abu38334 Protein e
7	34	97.1	474	ABU24881	Abu24881 Protein e
8	34	97.1	475	ABP30560	Abp30560 Streptoco
9	34	97.1	475	ABU40245	Abu40245 Protein e
10	34	97.1	475	ABU29756	Abu29756 Protein e
11	34	97.1	475	ADS24700	Ads24700 Bacterial
12	34	97.1	475	ADV87906	Adv87906 Streptoco
13	34	97.1	475	ADV81356	Adv81356 Streptoco
14	34	97.1	475	ADV79159	Adv79159 Streptoco
15	34	97.1	478	ADC97241	Adc97241 E. faeciu
16	34	97.1	479	ABP26968	Abp26968 Streptoco
17	34	97.1	490	ABB55389	Abb55389 Lactococc
18	34	97.1	496	ABB55385	Abb55385 Lactococc
19	34	97.1	499	ABO74582	Abu74582 Pseudomon
20	34	97.1	506	ABU22414	Abu22414 Protein e
21	34	97.1	585	ADA49403	Ada49403 Multi-epi
22	34	97.1	585	ADO24081	Ado24081 Epigene c
23	34	97.1	585	ADZ40583	Adz40583 HIV-TC mu
24	34	97.1	865	ABO70593	Abu70593 Pseudomon

25	33	94.3	10	5	ABP53931	Abp53931 VEGFR-3 b
26	33	94.3	10	5	ABP53932	Abp53932 VEGFR-3 b
27	33	94.3	69	4	AAO13595	Aao13595 Human pol
28	33	94.3	116	2	AAR15437	Aar15437 Heavy Cha
29	33	94.3	116	6	ABO27261	Abo27261 ICAM-1 bi
30	33	94.3	116	6	ABO27269	Abo27269 ICAM-1 bi
31	33	94.3	116	6	ABO27263	Abo27263 ICAM-1 bi
32	33	94.3	116	6	ABO27259	Abo27259 ICAM-1 bi
33	33	94.3	116	6	ABO27255	Abo27255 ICAM-1 bi
34	33	94.3	116	6	ABO27277	Abo27277 Humanised
35	33	94.3	116	6	ABO27273	Abo27273 Murine 1A
36	33	94.3	116	6	ABO27257	Abo27257 ICAM-1 bi
37	33	94.3	116	6	ABO27271	Abo27271 ICAM-1 bi
38	33	94.3	116	6	ABO27267	Abo27267 ICAM-1 bi
39	33	94.3	117	6	ABO27265	Abo27265 ICAM-1 bi
40	33	94.3	118	7	ADJ95639	Adj95639 Insulin-1
41	33	94.3	118	9	ADZ08201	Adz08201 IGF-speci
42	33	94.3	118	9	ADZ08173	Adz08173 IGF-speci
43	33	94.3	118	9	ADZ08158	Adz08158 IGF-speci
44	33	94.3	118	9	ADZ58532	Adz58532 VEGF rece
45	33	94.3	119	8	ADL11890	Adl11890 CDR trans

ALIGNMENTS

RESULT 1
AAB99759
ID AAB99759 standard; peptide; 10 AA.
XX
AC AAB99759;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rhesus D antibody binding peptide SEQ ID NO:4.
XX
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;
KW idiopathic thrombocytopenic purpura; immunoglobulin.
XX
OS Homo sapiens.
XX
PN EP1106625-A1.
XX
PD 13-JUN-2001.
XX
PF 17-NOV-1999; 99EP-00122858.
XX
PR 17-NOV-1999; 99EP-00122858.
XX
PA (ZLBB-) ZLB BIOPLASMA AG.
XX
PI Miescher S, Hofmann A, Fisch I;
XX
DR WPI; 2001-383568/41.
XX
PT Novel peptides capable of binding Rhesus D antibodies are used to
PT manufacture an agent for the diagnosis, therapy or prophylaxis of
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
PT newborn (HDN).
XX
PS Claim 1; Page 12; 19pp; English.
XX
CC The present sequence represents a peptide capable of binding Rhesus D
CC antibodies (I). Also described in the present invention are: (1) a
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
CC (II) operably linked to an expression control system; (3) a cell (IV)
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
CC peptides having immunologic properties of Rhesus D protein epitopes
CC comprising subjecting an antibody/antibody fragment recognising an
CC epitope of Rhesus D protein to several panning rounds with a phage
CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
CC manufacture an agent for the diagnosis, therapy or prophylaxis of
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
CC or removed from body fluids or immunoglobulin preparations. Using (I) as
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
CC with foreign erythrocytes thereby avoiding the risk of transmission of
CC viral diseases like AIDS and hepatitis B
XX
SQ Sequence 10 AA;

Query Match 97.1%; Score 34; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
||| |
Db 1 GYWSAKW 7

RESULT 2
AAB99769
ID AAB99769 standard; peptide; 12 AA.

XX AAB99769;
AC
XX 21-SEP-2001 (first entry)
XX Rhesus D antibody related peptide #5.

DE Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
XX anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;
KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Disulfide-bond 1..12

XX EP1106625-A1.

XX 13-JUN-2001.

XX 17-NOV-1999; 99EP-00122858.

XX 17-NOV-1999; 99EP-00122858.

XX (ZLBB-) ZLB BIOPLASMA AG.

XX Miescher S, Hofmann A, Fisch I;

DR WPI; 2001-383568/41.

XX Novel peptides capable of binding Rhesus D antibodies are used to
PT manufacture an agent for the diagnosis, therapy or prophylaxis of
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
PT newborn (HDN).

XX Example 1; Page 8; 19pp; English.

PS The present invention describes peptides capable of binding Rhesus D
XX antibodies (I). Also described in the present invention are: (1) a
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
CC (II) operably linked to an expression control system; (3) a cell (IV)
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
CC peptides having immunologic properties of Rhesus D protein epitopes
CC comprising subjecting an antibody/antibody fragment recognising an
CC epitope of Rhesus D protein to several panning rounds with a phage

CC display library, and identifying immunogenic peptide sequences which are
CC mimotopes which differ in their amino acid sequence from the amino acid
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
CC manufacture an agent for the diagnosis, therapy or prophylaxis of
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
CC or removed from body fluids or immunoglobulin preparations. Using (I) as
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
CC with foreign erythrocytes thereby avoiding the risk of transmission of
CC viral diseases like AIDS and hepatitis B. The present sequence represents
CC an anti-Rhesus D (RhD) antibody related peptide which is used in an
XX example from the present invention
SQ Sequence 12 AA;

Query Match 97.1%; Score 34; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
||| |
Db 2 GYWSAKW 8

RESULT 3
AAU03644
ID AAU03644 standard; protein; 452 AA.

XX AAU03644;

XX 12-SEP-2001 (first entry)

XX Group B Streptococcus antigenic protein, ID-119.

DE Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
XX meningitis; neonate; antigenic; vaccine; infection; genital tract;
KW capsid polysaccharide vaccination.

XX Streptococcus agalactiae.

XX WO200132882-A2.

XX 10-MAY-2001.

XX 07-SEP-2000; 2000WO-GB003437.

XX 07-SEP-1999; 99GB-00021125.

XX (MICR-) MICROBIAL TECHNIKS LTD.

XX Le Page RWF, Wells JM, Hanniffy SB;

XX WPI; 2001-316444/33.
DR N-PSDB; AAS07061.

XX New polypeptides derived from Streptococcus agalactiae are useful to
PT provide detection of, and vaccination against, Group B Streptococcus
PT infections, particularly to prevent infection in neonates.

PS Claim 1; Fig 1; 178pp; English.

XX AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
CC agalactiae) amino acid sequences of the invention.. S. agalactiae is an
CC encapsulated bacterium which is a major pathogen of humans causing sepsis
CC and meningitis in neonates as well as adults. The S. agalactiae antigenic
CC polypeptides are used to vaccinate against Group B Streptococcus
CC infections, particularly to prevent infection in new born children
CC arising from the maternal genital tract. An immunogenic composition is
CC useful in the preparation of a medicament for the treatment or
CC prophylaxis of Group B Streptococcus infection. The invention does not
CC have the disadvantages of varied response rate associated with prior art

CC capsid polysaccharide vaccination against Group B Streptococcus
XX
SQ Sequence 452 AA;

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
| | | | |
Db 92 GYWLSAW 98

RESULT 4
ABU21589
ID ABU21589 standard; protein; 466 AA.
XX
AC ABU21589;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #7116.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Burkholderia fungorum.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA25459.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 49513; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 466 AA;

Query Match 97.1%; Score 34; DB 6; Length 466;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
| | | | |
Db 86 GYVVSAM 92

RESULT 5
ADS44861
ID ADS44861 standard; protein; 469 AA.
XX
AC ADS44861;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23291.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 23291; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 469 AA;

Query Match 97.1%; Score 34; DB 8; Length 469;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 97 GYVVASW 103

RESULT 6
ABU38334
ID ABU38334 standard; protein; 472 AA.

AC ABU38334;
XX
DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #23861.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Pseudomonas aeruginosa.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA42204.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 66258; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 472 AA;

Query Match 97.1%; Score 34; DB 6; Length 472;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 94 GYWISAW 100

RESULT 7
ABU24881

ID ABU24881 standard; protein; 474 AA.

XX ABU24881;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #10408.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Clostridium botulinum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA28751.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 52805; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 474 AA;

Query Match 97.1%; Score 34; DB 6; Length 474;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 95 GYWLSAW 101

RESULT 8
ABP30560
ID ABP30560 standard; protein; 475 AA.
XX
AC ABP30560;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 10296.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.
PR 07-MAR-2001; 2001GB-00005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI; 2002-352536/38.
DR N-PSDB; ABN71191.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 4161; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 5; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 92 GYWLSAW 98

RESULT 9
ABU40245
ID ABU40245 standard; protein; 475 AA.
XX
AC ABU40245;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by prokaryotic essential gene #25772.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Pseudomonas putida.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX

PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA44115.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 68169; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
||| |
Db 93 GYWISAW 99

RESULT 10
ABU29756
ID ABU29756 standard; protein; 475 AA.
XX
AC ABU29756;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #15283.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Enterococcus faecium.
XX
PN WO200277183-A2.
XX

PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA33626.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 57680; 1766pp; English.
CC
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
||| |
Db 95 GYWLSAW 101

RESULT 11
ADS24700
ID ADS24700 standard; protein; 475 AA.
XX
AC ADS24700;
XX

DT 02-DEC-2004 (first entry)
XX Bacterial polypeptide #13733.
DE
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
DR New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 13733; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 93 GYWISAW 99

RESULT 12
ADV87906
ID ADV87906 standard; protein; 475 AA.
XX
XX ADV87906;
AC
XX 24-FEB-2005 (first entry)
DT
XX Streptococcus agalactiae protein sequence, SEQ ID 300.
DE
XX Antibacterial; Vaccine; bacterial infection.
KW
XX Streptococcus agalactiae.
OS
XX FR2824074-A1.
PN
XX 31-OCT-2002.
PD
XX 26-APR-2001; 2001FR-00005642.
PF
XX 26-APR-2001; 2001FR-00005642.
PR
XX (INSP) INST PASTEUR.
PA (CNRS.) CNRS CENT NAT RECH SCI.
PA
XX Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
PI WPI; 2004-101891/11.
XX
DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX and identification of therapeutic targets.
XX
PS Claim 6; SEQ ID NO 300; 2687pp; French.
XX
XX The present invention relates to novel Streptococcus agalactiae
CC nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
CC agalactiae involved in the synthesis of amino acids, cell membranes,
CC intermediate (central) metabolism, energetic metabolism, fatty acid and
CC phospholipid metabolism, nucleotide metabolism including purines,
CC pyrimidines and/or nucleosides, regulatory functions, replication,
CC transcription, translation, protein transport, adaptation to atypical
CC conditions, sensitivity to medicines and/or analogues, functions related
CC to transporters, biosynthesis of cofactors, prosthetic groups and
CC transporters, cell membrane proteins and cellular machinery. (I) are
CC useful for the detection and/or amplification of nucleic acids.
CC Pharmaceutical composition comprising (I) or (II) are useful for
CC treatment of a bacterial S. agalactiae infection. Note: WO200292818A2 is
CC equivalent for the present basic patent FR2824074A1. WO200292818A2
CC contains 6617 sequence whereas the present patent only contains 2344
CC sequences.
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 92 GYWLSAW 98

RESULT 13
ADV81356
ID ADV81356 standard; protein; 475 AA.
XX
XX ADV81356;
AC
XX 24-FEB-2005 (first entry)
DT

XX	Streptococcus agalactiae protein, SEQ ID 2497.	XX	21-NOV-2002.
DE	Antibacterial; vaccine; bacterial infection.	XX	26-APR-2002; 2002WO-IB003059.
XX	Streptococcus agalactiae.	XX	26-APR-2001; 2001FR-00005642.
KW		XX	(INSP) INST PASTEUR.
XX		PA	(CNRS) CNRS CENT NAT RECH SCI.
OS		XX	Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
PN		PI	Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX		XX	WPI; 2004-101891/11.
PD		XX	Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX		PT	agalactiae for the development of vaccines, diagnostic tools, DNA chips
PN		PT	and identification of therapeutic targets.
XX		PS	Claim 6; SEQ ID NO 2497; 439pp; French.
PF		XX	The present invention relates to novel Streptococcus agalactiae
XX		CC	nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
PR		CC	novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
XX		CC	nucleotide sequences encode polypeptides of S. agalactiae involved in the
XX		CC	synthesis of amino acids, cell membranes, intermediate (central)
XX		CC	metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
XX		CC	nucleotide metabolism including purines, pyrimidines and/or nucleosides,
XX		CC	regulatory functions, replication, transcription, translation, protein
XX		CC	transport, adaptation to atypical conditions, sensitivity to medicines
XX		CC	and/or analogues, functions related to transposons, biosynthesis of
XX		CC	cofactors, prosthetic groups and transporters, cell membrane proteins and
XX		CC	cellular machinery. (I) are useful for the detection and/or amplification
XX		CC	of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
XX		CC	useful for treatment of a bacterial S. agalactiae infection. The complete
XX		CC	genome of Streptococcus agalactiae is given in ADV81204. Note: The
XX		CC	present patent is an equivalent for the basic patent FR2824074A1, which
XX		CC	contains only 2344 sequences.
XX		XX	Sequence 475 AA;
SQ		SQ	Sequence 475 AA;
			Query Match 97.1%; Score 34; DB 8; Length 475;
			Best Local Similarity 57.1%; Pred. No. 4.6e+02;
			Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 GYWXXXW 7		
Db	92 GYWLSAW 98		
			RESULT 14
			ADV79159
ID	ADV79159 standard; protein; 475 AA.		
XX			Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX			abdominal-pelvic infection.
AC	ADV79159;		
XX			Enterococcus faecium.
XX			US6583275-B1.
DT	24-FEB-2005 (first entry)		
XX			24-JUN-2003.
DE	Streptococcus agalactiae protein, SEQ ID 300.		
XX			30-JUN-1998; 98US-00107532.
KW	Antibacterial; vaccine; bacterial infection.		
XX			02-JUL-1997; 97US-0051571P.
OS	Streptococcus agalactiae.		
XX			14-MAY-1998; 98US-0085598P.
PN	WO200292818-A2.		

XX (GENO-) GENOME THERAPEUTICS CORP.
PA Doucette-Stamm LA, Bush D;
XX WPI; 2003-799836/75.
PI N-PSDB; ADC93587.
XX
DR New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
PS Example 1; SEQ ID NO 6868; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX
SQ Sequence 478 AA;

Query Match 97.1%; Score 34; DB 7; Length 478;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GYWXXXW 7
| | | | |
Db 98 GYWLSAW 104

Search completed: May 2, 2006, 08:54:55
Job time : 78.9535 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 12.6977 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	72	T03190	hypothetical prote
2	34	97.1	108	S12193	hypothetical prote
3	34	97.1	345	T37139	hypothetical prote
4	34	97.1	469	D70048	ABC transporter (a
5	34	97.1	472	E83497	probable amino aci
6	34	97.1	475	T46745	arginine/ornithine
7	34	97.1	482	JH0110	arginine/ornithine
8	34	97.1	490	C86879	arginine/ornithine
9	34	97.1	497	G86878	arginine/ornithine
10	33	94.3	142	C34903	Ig heavy chain pre
11	33	94.3	227	S73905	CDPdiacylglycerol-
12	33	94.3	250	A69843	hypothetical prote
13	33	94.3	289	G72215	oligopeptide ABC t
14	33	94.3	360	AE2047	hypothetical prote
15	33	94.3	441	C95307	probable transport
16	33	94.3	508	C95282	probable ABC trans
17	33	94.3	517	AI3201	hypothetical prote
18	33	94.3	519	E83268	probable carbohydr
19	33	94.3	534	T15414	hypothetical prote
20	33	94.3	535	B95952	probable dipeptide
21	33	94.3	541	AC2392	hypothetical prote
22	33	94.3	563	AH2975	hypothetical prote
23	33	94.3	563	C98307	opha protein limpo
24	33	94.3	592	T15413	hypothetical prote
25	33	94.3	778	T31037	hypothetical prote
26	33	94.3	1502	T42216	multidrug resistan
27	32	91.4	71	S22905	lysis protein S -
28	32	91.4	83	E69903	hypothetical prote
29	32	91.4	187	G83047	hypothetical prote

30	32	91.4	218	2	S76385	hypothetical prote
31	32	91.4	218	2	D87264	hypothetical prote
32	32	91.4	257	2	E75325	probable mccf prot
33	32	91.4	261	2	JC5806	aquaporin 8 - mous
34	32	91.4	263	2	JC5622	aquaporin 8 - rat
35	32	91.4	271	2	F83188	phosphatidate cyti
36	32	91.4	271	2	JC4832	phosphatidate cyti
37	32	91.4	282	2	H95869	probable sugar ABC
38	32	91.4	286	2	E88690	protein F41H10.7 [
39	32	91.4	344	2	C82611	hypothetical prote
40	32	91.4	447	2	H97146	siderophore/Surfac
41	32	91.4	448	2	AB0301	conserved hypothet
42	32	91.4	466	2	T35164	probable secreted
43	32	91.4	519	2	S77572	oligopeptide trans
44	32	91.4	536	2	G95389	probable ABC trans
45	32	91.4	631	2	B86233	hypothetical prote

ALIGNMENTS

RESULT 1

T03190
hypothetical protein 72B - rice mitochondrion
C;Species: mitochondrion Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03190
R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existe
A;Reference number: Z14841; MUID:95211382; PMID:7545979
A;Accession: T03190
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <ITA>
A;Cross-references: UNIPROT:Q35302; UNIPARC:UPI000009746F; EMBL:D32052; NID:g769704; E
A;Experimental source: cultivar Nipponbare
C;Genetics:
A;Genome: mitochondrion
C;Keywords: mitochondrion

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 34 GYWSSHW 40

RESULT 2

S12193
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1
C;Species: Thiobacillus ferrooxidans
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S12193
R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidar
A;Reference number: S12188; MUID:91125140; PMID:2280689
A;Accession: S12193
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <DRO>
A;Cross-references: UNIPROT:P20088; UNIPARC:UPI000013B9EC; EMBL:X52699; NID:g48158; P:
C;Genetics:
A;Genome: plasmid pTF1

Query Match 97.1%; Score 34; DB 2; Length 108;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7


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Db      89 GYWRSSW 95
| || |
RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37139
R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <HAR>
A;Cross-references: UNIPROT:Q9S1R7; UNIPARC:UPI00000DB3A4; EMBL:AL109972; PIDN:CAB53264.
A;Experimental source: strain A3(2)
C;Genetics:
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: D70048
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D70048
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KUN>
A;Cross-references: UNIPROT:O32204; UNIPARC:UPI0000060A54; GB:Z99121; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: yvsh
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      97 GYVVASW 103

RESULT 5
E83497
probable amino acid permease PAl194 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pat
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
A;Cross-references: UNIPROT:Q9I4E4; UNIPARC:UPI00000C529E; GB:AE004549; GB:AE004091; N
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PAl194
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      94 GYWISAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: T46745
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez
J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes o
A;Reference number: Z23141; MUID:98361904; PMID:9696763
A;Accession: T46745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Cross-references: UNIPROT:O53092; UNIPARC:UPI0000125DAC; EMBL:AJ001330; NID:92764610
C;Genetics:
A;Gene: arcD
C;Function:
A;Description: necessary for arginine transport; involved in ornithine-arginine exchan
A;Pathway: arginine catabolism
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      94 GYWLSAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C;Accession: JH0110; A82999
R;Luethi, E.; Baur, H.; Gamper, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa co
A;Reference number: JH0110; MUID:90236296; PMID:2158926
A;Accession: JH0110
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Db      89 GYWRSSW 95
| || |
RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37139
R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <HAR>
A;Cross-references: UNIPROT:Q9S1R7; UNIPARC:UPI00000DB3A4; EMBL:AL109972; PIDN:CAB53264.
A;Experimental source: strain A3(2)
C;Genetics:
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: D70048
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D70048
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KUN>
A;Cross-references: UNIPROT:O32204; UNIPARC:UPI0000060A54; GB:Z99121; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: yvsh
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      97 GYVVASW 103

RESULT 5
E83497
probable amino acid permease PAl194 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pat
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
A;Cross-references: UNIPROT:Q9I4E4; UNIPARC:UPI00000C529E; GB:AE004549; GB:AE004091; N
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PAl194
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      94 GYWISAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: T46745
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez
J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes o
A;Reference number: Z23141; MUID:98361904; PMID:9696763
A;Accession: T46745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Cross-references: UNIPROT:O53092; UNIPARC:UPI0000125DAC; EMBL:AJ001330; NID:92764610
C;Genetics:
A;Gene: arcD
C;Function:
A;Description: necessary for arginine transport; involved in ornithine-arginine exchan
A;Pathway: arginine catabolism
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      ||| |
Db      94 GYWLSAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C;Accession: JH0110; A82999
R;Luethi, E.; Baur, H.; Gamper, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa co
A;Reference number: JH0110; MUID:90236296; PMID:2158926
A;Accession: JH0110
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A;Molecule type: DNA
A;Residues: 1-482 <LUE>
A;Cross-references: UNIPROT:P18275; UNIPARC:UPI00000618AA; GB:M33223; NID:G151030; PIDN:
A;Experimental source: strain PA01
A;Note: the gene encoding this protein is located upstream of the arcABC genes which encode
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A82999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <STO>
A;Cross-references: UNIPARC:UPI00000618AA; GB:AE004930; NID:G9951472; PIDN:
A;Experimental source: strain PA01
C;Genetics:
A;Gene: arcD; PA5170
C;Superfamily: ecotropic retrovirus receptor protein
C;Keywords: transmembrane protein

Query Match 97.1%; Score 34; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 94 GYWISAW 100

RESULT 8
C86879
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C;Accession: C86879
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissensbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <STO>
A;Cross-references: UNIPROT:Q9CE15; UNIPARC:UPI000006B99; GB:AE005176; PID:G12725084; P
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcD1
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 490;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 93 GYWLAW 99

RESULT 9
G86878
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C;Accession: G86878
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissensbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86878
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-497 <STO>
A;Cross-references: UNIPROT:Q9CE19; UNIPARC:UPI000006B95; GB:AE005176; PID:G12725079;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcD2
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 497;
Best Local Similarity 57.1%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 93 GYWISAW 99

RESULT 10
C34903
Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C;Accession: C34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-r
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
A;Cross-references: UNIPARC:UPI0000176C0F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 94.3%; Score 33; DB 2; Length 142;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 126 GYWFAYW 132

RESULT 11
S73905
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - M
N;Alternate names: hypothetical protein A65_orf227
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S73905
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoni
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73905
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-227 <HIM>
A;Cross-references: UNIPROT:P75520; UNIPARC:UPI0000131886; EMBL:AE000057; GB:U00089; N
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: pgsA
A;Genetic code: SGC3
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C;Keywords: transferase

Query Match 94.3%; Score 33; DB 2; Length 227;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

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Db          84 GYWARXW 90

RESULT 12
A69843
hypothetical protein yjba - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69843
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: A69843
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-250 <KUN>
A;Cross-references: UNIPROT:O31597; UNIPARC:UPI0000060207; GB:Z99110; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: yjba
C;Superfamily: Bacillus subtilis hypothetical protein yjba

Query Match          94.3%; Score 33; DB 2; Length 250;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 GYWXXXW 7
          |||||
          185 GYWTETW 191

Db

RESULT 13
G72215
oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72215
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-289 <ARN>
A;Cross-references: UNIPROT:Q9X270; UNIPARC:UPI000000D385E; GB:AE001813; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1748
C;Superfamily: oligopeptide permease protein oppB

Query Match          94.3%; Score 33; DB 2; Length 289;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 GYWXXXW 7
          |||||

Db          84 GYWARXW 90

RESULT 14
AE2047
hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2047
R;Kaneoko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2047
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <KUR>
A;Cross-references: UNIPROT:Q8YVP3; UNIPARC:UPI000000CE269; GB:BA000019; PIDN:BA073630.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1931

Query Match          94.3%; Score 33; DB 2; Length 360;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 GYWXXXW 7
          |||||
          127 GYWSYGW 133

Db

RESULT 15
C95307
probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) me
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004
C;Accession: C95307
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <KUR>
A;Cross-references: UNIPROT:Q92ZT6; UNIPARC:UPI000000CB08F; GB:AE006469; PIDN:AAK65021.7
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, F
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma0684
A;Genome: plasmid
C;Superfamily: ecotropic retrovirus receptor protein

Query Match          94.3%; Score 33; DB 2; Length 441;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          1 GYWXXXW 7
          |||||
          92 GYWISIW 98

Db
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us-10-046-922-67.rpr

Tue May 2 12:32:42 2006

Search completed: May 2, 2006, 08:56:19
Job time : 12.6977 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 79.2791 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length:- 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
- and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	97.1	72	2	Q35302_ORYSA	Q35302 oryza sativ
2	34	97.1	108	1	YML2_THIFE	P20088 thioabacillu
3	34	97.1	130	2	Q7U395_PROMP	Q7u395 prochloroco
4	34	97.1	236	2	Q9WGW9_9HIV1	Q9wgw9 human immun
5	34	97.1	253	2	Q32816_LACLC	Q32816 lactococcus
6	34	97.1	294	2	Q8ET30_OCEIH	Q8et30 oceanobacil
7	34	97.1	333	2	Q6F6U4_ACIAD	Q6f6u4 acinetobact
8	34	97.1	345	2	Q9S1R7_STRCO	Q9slr7 streptomyce
9	34	97.1	451	2	Q62C74_BURMA	Q62c74 burkholderi
10	34	97.1	459	2	Q9KGV3_LACLA	Q9kgv3 lactococcus
11	34	97.1	464	2	Q84DL5_OENOE	Q84dl5 oenococcus
12	34	97.1	465	2	Q6I3F7_BACAN	Q6i3f7 bacillus an
13	34	97.1	465	2	Q4MN56_BACCCE	Q4mn56 bacillus ce
14	34	97.1	465	2	Q81HZ7_BACCR	Q81hz7 bacillus ce
15	34	97.1	465	2	Q63G16_BACC2	Q63g16 bacillus ce
16	34	97.1	465	2	Q6HNI4_BACHK	Q6hni4 bacillus th
17	34	97.1	465	2	Q73DL5_BACC1	Q73dl5 bacillus ce
18	34	97.1	465	2	Q81V71_BACAN	Q81v71 bacillus li
19	34	97.1	469	2	Q65F15_BACLD	Q65f15 bacillus li
20	34	97.1	469	2	Q6TK71_STRRT	Q6tk71 streptococc
21	34	97.1	469	2	Q32204_BACSU	Q32204 bacillus su
22	34	97.1	471	2	Q6HP27_BACHK	Q6hp27 bacillus th
23	34	97.1	471	2	Q73E85_BACC1	Q73e85 bacillus ce
24	34	97.1	471	2	Q81IH9_BACCR	Q81ih9 bacillus ce
25	34	97.1	472	2	Q9I4E4_PSEAE	Q9i4e4 pseudomonas
26	34	97.1	473	2	Q7NRJ8_CHRVO	Q7nrj8 chromobacte
27	34	97.1	475	1	ARCD_LACSK	O53092 lactobacill
28	34	97.1	475	2	Q4ZT00_PSESY	Q4zt00 pseudomonas
29	34	97.1	475	2	Q4K7R6_PSEF5	Q4k7r6 pseudomonas
30	34	97.1	475	2	Q4K7R5_PSEF5	Q4k7r5 pseudomonas
31	34	97.1	475	2	Q88P50_PSEPK	Q88p50 pseudomonas

32	34	97.1	475	2	Q88P51_PSEPK	Q88p51 pseudomonas
33	34	97.1	475	2	Q8DWP9_STRAS	Q8dwp9 streptococc
34	34	97.1	475	2	Q8E2J7_STRAS	Q8e2j7 streptococc
35	34	97.1	478	1	ARCD_CLOPE	Q46170 clostridium
36	34	97.1	482	1	ARCD_PSEAE	P18275 pseudomonas
37	34	97.1	486	2	Q63U74_BURPS	Q63u74 burkholderi
38	34	97.1	486	2	Q62KE0_BURMA	Q62ke0 burkholderi
39	34	97.1	490	2	Q9CE15_LACLA	Q9ce15 lactococcus
40	34	97.1	496	2	Q63L96_BURPS	Q63l96 burkholderi
41	34	97.1	497	2	Q9KGV0_LACLA	Q9kgv0 lactococcus
42	34	97.1	497	2	Q9CE19_LACLA	Q9ce19 lactococcus
43	34	97.1	526	2	Q9K574_9LACT	Q9k574 lactococcus
44	34	97.1	552	2	Q5LSW7_SILPO	Q5lsw7 silicibacte
45	34	97.1	753	2	Q4TSN3_9SPHN	Q4tsn3 erythrobact

ALIGNMENTS

RESULT 1

Q35302_ORYSA
ID Q35302_ORYSA PRELIMINARY; PRT; 72 AA.
AC Q35302;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE ORF72B.
OS Oryza sativa (japonica cultivar-group).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,
RA Il'in Y.V.;
RT "Structure of long and short copies of the mobile dispersed gene MDG3
of Drosophila melanogaster.";
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95308541; PubMed=7788722; DOI=10.1007/BF00313433;
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyura M.,
RA Hirai A.;
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is
transcribed from alternative promoters.";
RL Curr. Genet. 27:184-189(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95211382; PubMed=7545979;
RA Itadani H., Wakasugi T., Sugita M., Sugiyura M., Nakazono M., Hirai A.;
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
RL Plant Cell Physiol. 35:1239-1244(1994).
DR EMBL; D32052; BAA06811.1; -; Genomic_DNA.
DR PIR; T03190; T03190.
DR Gramene; Q35302; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 34 GYWSSHW 40

RESULT 2

YML2_THIFE
ID YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3'region (ORF 4).
OS Thiobacillus ferrooxidans.
OC Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; X52699; CAA36930.1; -; Genomic_DNA.
DR PIR; S12193; S12193.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 97.1%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 89 GYWRSSW 95
| | | | |

RESULT 3
Q7U395_PROMP PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf).
GN OrderedLocusNames=PM1067;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19526.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 7 GYWTLAW 13
| | | | |

RESULT 4
Q9WGW9_9HIV1 PRELIMINARY; PRT; 236 AA.
AC Q9WGW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -; Genomic_DNA.
DR HSSP; P03366; 1HRH.
DR SMR; Q9WGW9; 1-236.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PSS0879; RNase_H; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 129 GYWQATW 135
| | | | |

RESULT 5
O32816_LACLC PRELIMINARY; PRT; 253 AA.
ID O32816_LACLC
AC O32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MG1363;
RX MEDLINE=97369814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
by ISS1 transposition.";
RL J. Bacteriol. 179:4473-4479(1997).
DR EMBL; U81991; AAC45504.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
KW Transmembrane.
FT NON TER 253 253
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 93 GYWLSAW 99

RESULT 6
Q8ET30_OCEIH PRELIMINARY; PRT; 294 AA.
AC Q8ET30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter permease.
GN OrderedLocusNames=OB0434;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC12390.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR InterPro; IPR001626; ABC_3.
DR Pfam; PF00950; ABC-3; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 294 AA; 31323 MW; F75E0F22EA4071A CRC64;

Query Match 97.1%; Score 34; DB 2; Length 294;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 244 GYWIATW 250

RESULT 7
Q6F6U4_ACIA4 PRELIMINARY; PRT; 333 AA.
ID Q6F6U4_ACIA4

AC Q6F6U4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transporter; putative sodium/bile acid transporter family
protein.
DE OrderedLocusNames=ACIAD3583;
GN Acinetobacter sp. (strain ADP1).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP1;
RX PubMed=15514110; DOI=10.1093/nar/gkh910;
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CR543861; CAG70223.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008508; F:bile acid:sodium symporter activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR002657; BilAc/Na_symport.
DR Pfam; PF01758; SBF; 1.
KW Complete proteome.
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 333;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 252 GYWASRW 258

RESULT 8
Q9S1R7_STRCO PRELIMINARY; PRT; 345 AA.
ID Q9S1R7_STRCO
AC Q9S1R7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCO0224.
GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03C;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939104; CAB53264.1; -; Genomic_DNA.
DR PIR; T37139; T37139.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 147 GYWAARW 153

RESULT 9
Q62C74 BURMA PRELIMINARY; PRT; 451 AA.
ID Q62C74 BURMA PRELIMINARY; PRT; 451 AA.
AC Q62C74;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Amino acid permease.
GN OrderedLocusNames=BMAA1038;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.B., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000011; AAU46467.1; -; Genomic_DNA.
DR TIGR; BMAA1038; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
KW SEQUENCE 451 AA; 47344 MW; ED2DIADDEB0C4A55 CRC64;
SQ

Query Match 97.1%; Score 34; DB 2; Length 451;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 116 GYVWSAW 122

RESULT 10
Q9KGV3 LACLA PRELIMINARY; PRT; 459 AA.
ID Q9KGV3 LACLA PRELIMINARY; PRT; 459 AA.
AC Q9KGV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ArcD1.
GN Name=arcD1;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ML3;
RA Chou L., Weimer B., Xie Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ML3;
RC Chou L.-S., Weimer B., Xie Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282249; AAF86987.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;
Query Match 97.1%; Score 34; DB 2; Length 459;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 92 GYWLSAW 98

RESULT 11
Q84DL5 OENOE PRELIMINARY; PRT; 464 AA.
ID Q84DL5 OENOE PRELIMINARY; PRT; 464 AA.
AC Q84DL5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arginine/ornithine antiporter ArcD2.
GN Name=arcD2;
OS Oenococcus oeni (Leuconostoc oenos).
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.
OX NCBI_TaxID=1247;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23279;
RX MEDLINE=22519090; PubMed=12631210;
RX DOI=10.1046/j.1365-2672.2003.01907.x;
RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;
RT "Molecular characterization of Oenococcus oeni genes encoding proteins involved in arginine transport.";
RL J. Appl. Microbiol. 94:738-746(2003).
DR EMBL; AF541253; AAO83382.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;
Query Match 97.1%; Score 34; DB 2; Length 464;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 94 GYWLSSW 100

RESULT 12
Q6I3F7 BACAN PRELIMINARY; PRT; 465 AA.
ID Q6I3F7 BACAN PRELIMINARY; PRT; 465 AA.
AC Q6I3F7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)


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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BAS0596;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretttin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017225; AAT52924.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
DR Transmembrane; Transport.
KW SEQUENCE
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 96 GYWAANW 102

RESULT 13
Q4MN56_BACCE PRELIMINARY; PRT; 465 AA.
ID Q4MN56;
AC Q4MN56;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Arginine/ornithine antiporter.
GN Name=arcD; ORFNames=BCE_G9241_0606;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA001000024; EAL13575.1; -; Genomic DNA.
SQ SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
| | | |
Db 96 GYWAANW 102
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Db 96 GYWAANW 102
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RESULT 14
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ID Q81HZ7;
AC Q81HZ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arginine/ornithine antiporter.
GN OrderedLocusNames=BC0629;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017000; AAP07646.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
KW SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
| | | |
Db 96 GYWAANW 102

RESULT 15
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ID Q63G16;
AC Q63G16;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable arginine/ornithine antiporter protein.
GN Name=arcD;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretttin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU19700.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
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DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR022293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXKXW 7
Db 96 GYWAANW 102

Search completed: May 2, 2006, 08:46:46
Job time : 79.2791 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 19.8605 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXW 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	478	US-09-107-532A-6868	Sequence 6868, Ap
2	34	97.1	499	US-09-252-991A-23328	Sequence 23328, A
3	34	97.1	865	US-09-252-991A-19339	Sequence 19339, A
4	33	94.3	543	US-09-252-991A-18697	Sequence 18697, A
5	33	94.3	1498	US-09-792-616-9	Sequence 9, Appli
6	33	94.3	1503	US-09-792-616-3	Sequence 3, Appli
7	33	94.3	1503	US-09-647-140B-8	Sequence 8, Appli
8	32	91.4	88	US-09-902-540-12675	Sequence 12675, A
9	32	91.4	177	US-09-543-681A-7620	Sequence 7620, Ap
10	32	91.4	252	US-09-502-653-10	Sequence 10, Appl
11	32	91.4	263	US-09-610-906-12	Sequence 12, Appl
12	32	91.4	274	US-09-248-796A-15791	Sequence 15791, A
13	32	91.4	278	US-09-145-828A-11	Sequence 11, Appl
14	32	91.4	278	US-09-903-456-18	Sequence 18, Appl
15	32	91.4	278	US-09-624-670-17	Sequence 17, Appl
16	32	91.4	339	US-09-252-991A-26841	Sequence 26841, A
17	32	91.4	362	US-08-415-751-6	Sequence 6, Appli
18	32	91.4	367	US-09-248-796A-15188	Sequence 15188, A
19	32	91.4	492	US-09-107-532A-6945	Sequence 6945, Ap
20	32	91.4	500	US-09-252-991A-21214	Sequence 21214, A
21	31	88.6	185	US-10-808-807-12	Sequence 12, Appl
22	31	88.6	342	US-09-252-991A-32031	Sequence 32031, A
23	30	85.7	11	US-09-069-827A-87	Sequence 87, Appl
24	30	85.7	16	US-09-620-091-81	Sequence 81, Appl
25	30	85.7	519	US-09-198-452A-479	Sequence 479, App
26	30	85.7	519	US-09-438-185A-454	Sequence 454, App
27	30	85.7	654	US-09-252-991A-18441	Sequence 18441, A

28	30	85.7	2357	2	US-09-949-016-9656	Sequence 9656, Ap
29	29	82.9	26	2	US-09-962-756-1516	Sequence 1516, Ap
30	29	82.9	34	2	US-09-270-767-60715	Sequence 60715, A
31	29	82.9	35	2	US-09-082-279B-1191	Sequence 1191, Ap
32	29	82.9	35	2	US-09-315-304B-1191	Sequence 1191, Ap
33	29	82.9	35	2	US-09-834-784-1191	Sequence 1191, Ap
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36	29	82.9	35	2	US-09-350-841A-1191	Sequence 1191, Ap
37	29	82.9	55	2	US-09-621-976-7633	Sequence 7633, Ap
38	29	82.9	69	2	US-09-621-976-7239	Sequence 7239, Ap
39	29	82.9	139	2	US-09-252-991A-19685	Sequence 19685, A
40	29	82.9	142	2	US-09-252-991A-22994	Sequence 22994, A
41	29	82.9	197	2	US-09-543-681A-5312	Sequence 5312, Ap
42	29	82.9	227	2	US-09-489-039A-8752	Sequence 8752, Ap
43	29	82.9	255	2	US-09-270-767-45223	Sequence 45223, A
44	29	82.9	286	2	US-09-712-363-168	Sequence 168, Appl
45	29	82.9	291	2	US-10-272-490-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-107-532A-6868
; Sequence 6868, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:

US-09-107-532A-6868

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Query Match      97.1%; Score 34; DB 2; Length 478;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      98 GYWLSAW 104

RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match      97.1%; Score 34; DB 2; Length 499;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      111 GYWISAW 117

RESULT 3
US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19339
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19339

Query Match      97.1%; Score 34; DB 2; Length 865;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      487 GYWISAW 493

RESULT 4
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US-09-252-991A-18697
; Sequence 18697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18697
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697
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Query Match      94.3%; Score 33; DB 2; Length 543;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GYWXXXW 7
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Db      331 GYWMVSW 337
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RESULT 5
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9
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Query Match      94.3%; Score 33; DB 2; Length 1498;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GYWXXXW 7
      ||| |
Db      960 GYWLSLW 966
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RESULT 6
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match 94.3%; Score 33; DB 2; Length 1503;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 965 GYWLSLW 971

RESULT 7
US-09-647-140B-8
; Sequence 8, Application US/09647140B
; Patent No. 6803184
; GENERAL INFORMATION:
; APPLICANT: Fox Chase Cancer Center
; APPLICANT: Kruh, Gary D.
; APPLICANT: Lee, Kun
; APPLICANT: Belinsky, Martin G.
; APPLICANT: Bain, Lisa J.
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof
; FILE REFERENCE: FCCC 98-02
; CURRENT APPLICATION NUMBER: US/09/647,140B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US99/06644
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,759
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/095,153
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0.
; SEQ ID NO 8
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-647-140B-8

Query Match 94.3%; Score 33; DB 2; Length 1503;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 965 GYWLSLW 971

RESULT 8
US-09-902-540-12675
; Sequence 12675, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12675
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Myxococcus xanthus

US-09-902-540-12675

Query Match 91.4%; Score 32; DB 2; Length 88;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 48 GYWLDCW 54

RESULT 9
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7620

Query Match 91.4%; Score 32; DB 2; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 43 GYWVINW 49

RESULT 10
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schleim, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
US-09-502-653-10

Query Match 91.4%; Score 32; DB 2; Length 252;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;

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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      210 GYWEPAW 216

RESULT 11
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingner, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match      91.4%; Score 32; DB 2; Length 263;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      224 GYWDFHW 230

RESULT 12
US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

Query Match      91.4%; Score 32; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      84 GYWPITW 90

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer J.
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      108 GYWIFLW 114

RESULT 14
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
Db      108 GYWIFLW 114

RESULT 15
US-09-624-670-17
; Sequence 17, Application US/09624670
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Tue May 2 12:32:41 2006

Patent No. 6913916
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Das, Tapas
APPLICANT: Huang, Yung-Sheng
APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Thurmond, Jennifer M.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P2
CURRENT APPLICATION NUMBER: US/09/624,670
CURRENT FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 278
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-624-670-17

Query Match 91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
||| |
Db 108 GYWIFLW 114

Search completed: May 2, 2006, 08:58:26
Job time : 20.8605 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:23:40 ; Search time 65.1163 Seconds
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Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXXXW 7

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Searched: 1867569 seqs, 417829326 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	58	4	US-10-425-115-308836 Sequence 308836,
2	34	97.1	72	4	US-10-437-963-176036 Sequence 176036,
3	34	97.1	452	4	US-10-091-007-88 Sequence 88, Appl
4	34	97.1	466	4	US-10-282-122A-49513 Sequence 49513, A
5	34	97.1	469	4	US-10-369-493-23291 Sequence 23291, A
6	34	97.1	472	4	US-10-282-122A-66258 Sequence 66258, A
7	34	97.1	474	4	US-10-282-122A-52805 Sequence 52805, A
8	34	97.1	475	4	US-10-369-493-13733 Sequence 13733, A
9	34	97.1	475	4	US-10-282-122A-57680 Sequence 57680, A
10	34	97.1	475	4	US-10-282-122A-68169 Sequence 68169, A
11	34	97.1	506	4	US-10-282-122A-50338 Sequence 50338, A
12	34	97.1	585	3	US-09-894-018-87 Sequence 87, Appl
13	34	97.1	585	5	US-10-474-960A-87 Sequence 87, Appl
14	33	94.3	10	4	US-10-046-922-34 Sequence 34, Appl
15	33	94.3	10	4	US-10-046-922-35 Sequence 35, Appl
16	33	94.3	47	4	US-10-425-115-287762 Sequence 287762,
17	33	94.3	104	4	US-10-425-115-273234 Sequence 273234,
18	33	94.3	116	3	US-09-910-483-1 Sequence 1, Appli
19	33	94.3	116	3	US-09-910-483-5 Sequence 5, Appli
20	33	94.3	116	3	US-09-910-483-9 Sequence 9, Appli
21	33	94.3	116	3	US-09-910-483-13 Sequence 13, Appl
22	33	94.3	116	3	US-09-910-483-17 Sequence 17, Appl
23	33	94.3	116	3	US-09-910-483-21 Sequence 21, Appl
24	33	94.3	116	3	US-09-910-483-25 Sequence 25, Appl
25	33	94.3	116	3	US-09-910-483-29 Sequence 29, Appl
26	33	94.3	116	3	US-09-910-483-33 Sequence 33, Appl
27	33	94.3	116	3	US-09-910-483-37 Sequence 37, Appl

28	33	94.3	116	3	US-09-910-483-41	Sequence 41, Appl
29	33	94.3	116	3	US-09-910-483-43	Sequence 43, Appl
30	33	94.3	129	4	US-10-425-115-357518	Sequence 357518,
31	33	94.3	138	4	US-10-160-232-86	Sequence 86, Appl
32	33	94.3	138	4	US-10-160-232-90	Sequence 90, Appl
33	33	94.3	227	4	US-10-282-122A-64263	Sequence 64263, A
34	33	94.3	229	4	US-10-425-115-344695	Sequence 344695,
35	33	94.3	257	5	US-10-450-763-43035	Sequence 43035, A
36	33	94.3	296	4	US-10-156-761-9632	Sequence 9632, Ap
37	33	94.3	296	4	US-10-369-493-19811	Sequence 19811, A
38	33	94.3	466	4	US-10-369-493-16537	Sequence 16537, A
39	33	94.3	467	4	US-10-437-963-199114	Sequence 199114,
40	33	94.3	516	4	US-10-450-022-7	Sequence 7, Appli
41	33	94.3	526	4	US-10-450-022-4	Sequence 4, Appli
42	33	94.3	526	4	US-10-450-022-5	Sequence 5, Appli
43	33	94.3	526	5	US-10-450-185B-2	Sequence 2, Appli
44	33	94.3	526	5	US-10-450-185B-17	Sequence 17, Appl
45	33	94.3	526	5	US-10-433-747B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-425-115-308836
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308836
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44726C.1.pep
US-10-425-115-308836

Query Match 97.1% Score 34; DB 4; Length 58;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 49 GYWGASW 55

RESULT 2
US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036

Query Match 97.1%; Score 34; DB 4; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 34 GYSSHW 40

RESULT 3
US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited wells, Jeremy M
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 92 GYLSAW 98

RESULT 4
US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match 97.1%; Score 34; DB 4; Length 466;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 86 GYVSAW 92

RESULT 5
US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291

Query Match 97.1%; Score 34; DB 4; Length 469;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 97 GYVSAW 103

RESULT 6
US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

```

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66258
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258

Query Match          97.1%; Score 34; DB 4; Length 472;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      94 GYWISAW 100

RESULT 7
US-10-282-122A-52805
; Sequence 52805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52805
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-282-122A-52805

Query Match          97.1%; Score 34; DB 4; Length 474;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      95 GYWLAW 101

RESULT 8
US-10-369-493-13733
; Sequence 13733, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13733
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733

Query Match          97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GYWXXXW 7
Db      93 GYWISAW 99

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RESULT 9
US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57680
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57680

Query Match          97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      95 GYWLSAW 101

RESULT 10
US-10-282-122A-68169
; Sequence 68169, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57680
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57680

Query Match          97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      95 GYWLSAW 101
```

```
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68169
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68169

Query Match          97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      93 GYWLSAW 99

RESULT 11
US-10-282-122A-50338
; Sequence 50338, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68169
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68169
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50338
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-10-282-122A-50338

Query Match          97.1%; Score 34; DB 4; Length 506;
Best Local Similarity 57.1%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      124 GYWISAW 130

RESULT 12
US-09-894-018-87
; Sequence 87, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-09-894-018-87

Query Match          97.1%; Score 34; DB 3; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28

US-09-894-018-87
; Sequence 87, Application US/10474960A
; Publication No. US20040248113A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denise
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
; TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby
; FILE REFERENCE: 2060.0320004
; CURRENT APPLICATION NUMBER: US/10/474,960A
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/US02/09877
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/894,018
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
US-10-474-960A-87

Query Match          97.1%; Score 34; DB 5; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28

US-10-474-960A-87
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match          94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
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Db      22 GYWQATW 28
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Db ||| |
 2 GYWLTIW 8

RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. NO. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYWXXXW 7
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Db 2 GYWLTIW 8

Search completed: May 2, 2006, 09:32:39
Job time : 65.1163 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17; Search time 9.93023 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-67
Perfect score: 35
Sequence: 1 GYWXXW 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:
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6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:
7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1:
8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:
9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:
10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:
11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	464	11 US-11-087-099-1003	Sequence 1003, Ap
2	34	97.1	469	11 US-11-087-099-11321	Sequence 11321, A
3	34	97.1	471	11 US-11-188-298-19864	Sequence 19864, A
4	34	97.1	472	11 US-11-087-099-12291	Sequence 12291, A
5	34	97.1	475	11 US-11-087-099-1870	Sequence 1870, Ap
6	34	97.1	475	11 US-11-087-099-2298	Sequence 2298, Ap
7	34	97.1	475	11 US-11-087-099-7571	Sequence 7571, Ap
8	34	97.1	475	11 US-11-188-298-6764	Sequence 6764, Ap
9	34	97.1	476	11 US-11-087-099-1256	Sequence 1256, Ap
10	34	97.1	478	11 US-11-087-099-7019	Sequence 7019, Ap
11	34	97.1	478	11 US-11-087-099-9555	Sequence 9555, Ap
12	34	97.1	478	11 US-11-188-298-8872	Sequence 8872, Ap
13	34	97.1	482	11 US-11-087-099-4146	Sequence 4146, Ap
14	34	97.1	491	11 US-11-087-099-9097	Sequence 9097, Ap
15	33	94.3	119	11 US-11-250-411-97	Sequence 97, Appl
16	33	94.3	119	11 US-11-250-411-101	Sequence 101, Appl
17	33	94.3	138	11 US-11-250-411-86	Sequence 86, Appl
18	33	94.3	138	11 US-11-250-411-90	Sequence 90, Appl
19	33	94.3	441	11 US-11-087-099-2305	Sequence 2305, Ap
20	33	94.3	456	11 US-11-087-099-8799	Sequence 8799, Ap
21	33	94.3	474	11 US-11-087-099-10672	Sequence 10672, A

22	33	94.3	1023	9 US-10-995-561-968	Sequence 968, App
23	32	91.4	122	9 US-10-467-657-5906	Sequence 5906, Ap
24	32	91.4	445	11 US-11-079-463-8428	Sequence 8428, Ap
25	32	91.4	480	11 US-11-079-463-7586	Sequence 7586, Ap
26	32	91.4	566	11 US-11-188-298-3470	Sequence 3470, Ap
27	32	91.4	986	11 US-11-079-463-10025	Sequence 10025, A
28	31	88.6	10	11 US-11-129-741-3641	Sequence 3641, Ap
29	30	85.7	16	9 US-10-929-988-81	Sequence 81, Appl
30	30	85.7	2335	9 US-10-821-234-1610	Sequence 1610, Ap
31	29	82.9	347	9 US-10-506-454-1117	Sequence 1117, Ap
32	29	82.9	400	9 US-10-467-657-7096	Sequence 7096, Ap
33	29	82.9	488	11 US-11-087-099-7125	Sequence 7125, Ap
34	28	80.0	8	11 US-11-045-024-4376	Sequence 4376, Ap
35	28	80.0	8	11 US-11-045-024-4377	Sequence 4377, Ap
36	28	80.0	8	11 US-11-045-024-12720	Sequence 12720, A
37	28	80.0	8	11 US-11-045-024-12755	Sequence 12755, A
38	28	80.0	9	11 US-11-045-024-262	Sequence 262, App
39	28	80.0	9	11 US-11-045-024-263	Sequence 263, App
40	28	80.0	9	11 US-11-045-024-4500	Sequence 4500, Ap
41	28	80.0	9	11 US-11-045-024-4501	Sequence 4501, Ap
42	28	80.0	9	11 US-11-045-024-6570	Sequence 6570, Ap
43	28	80.0	9	11 US-11-045-024-6641	Sequence 6641, Ap
44	28	80.0	10	11 US-11-045-024-2129	Sequence 2129, Ap
45	28	80.0	10	11 US-11-045-024-2130	Sequence 2130, Ap

ALIGNMENTS

RESULT 1
US-11-087-099-1003
; Sequence 1003, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1003
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Oenococcus oeni
US-11-087-099-1003

Query Match 97.1%; Score 34; DB 11; Length 464;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXW 7
DB 94 GYWLSSW 100
RESULT 2
US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-087-099-11321
Query Match 97.1%; Score 34; DB 11; Length 469;

Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 97 GYVVASW 103

RESULT 3

US-11-188-298-19864
; Sequence 19864, Application US/11188298
; Publication No. US20060075522A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-21(53452)B

; CURRENT APPLICATION NUMBER: US/11/188,298

; CURRENT FILING DATE: 2005-07-22

; PRIOR APPLICATION NUMBER: 60/592,978

; PRIOR FILING DATE: 2004-07-31

; NUMBER OF SEQ ID NOS: 22569

; SEQ ID NO 19864

; LENGTH: 471

; TYPE: PRT

; ORGANISM: Bacillus cereus ATCC 14579

US-11-188-298-19864

Query Match 97.1%; Score 34; DB 11; Length 471;

Best Local Similarity 57.1%; Pred. No. 91;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 92 GYWLSAW 98

RESULT 4

US-11-087-099-12291

; Sequence 12291, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 12291

; LENGTH: 472

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa PAO1

US-11-087-099-12291

Query Match 97.1%; Score 34; DB 11; Length 472;

Best Local Similarity 57.1%; Pred. No. 91;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 94 GYWISAW 100

RESULT 5

US-11-087-099-1870

; Sequence 1870, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 1870

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Pseudomonas syringae pv. syringae B728a

US-11-087-099-1870

Query Match

Best Local Similarity 97.1%; Score 34; DB 11; Length 475;

Matches 4; Conservative 57.1%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

||| |

Db 93 GYWISAW 99

RESULT 6

US-11-087-099-2298

; Sequence 2298, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 2298

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Pseudomonas putida KT2440

US-11-087-099-2298

Query Match

Best Local Similarity 97.1%; Score 34; DB 11; Length 475;

Matches 4; Conservative 57.1%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

||| |

Db 93 GYWISAW 99

RESULT 7

US-11-087-099-7571

; Sequence 7571, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 7571

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Pseudomonas putida KT2440

US-11-087-099-7571

Query Match

Best Local Similarity 97.1%; Score 34; DB 11; Length 475;

Matches 4; Conservative 57.1%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

||| |

Db 93 GYWISAW 99

RESULT 8

US-11-188-298-6764

; Sequence 6764, Application US/11188298

; Publication No. US2006007552A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

```

; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match          97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      94 GYWLSAW 100

RESULT 9
US-11-087-099-1256
; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1256
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-11-087-099-1256

Query Match          97.1%; Score 34; DB 11; Length 476;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      95 GYWLSAW 101

RESULT 10
US-11-087-099-7019
; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7019
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-7019

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      98 GYWLSAW 104

US-11-087-099-9555
; Sequence 9555, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9555
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-087-099-9555

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      96 GYWLSAW 102

RESULT 12
US-11-188-298-8872
; Sequence 8872, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8872
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-188-298-8872

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      96 GYWLSAW 102

RESULT 13
US-11-087-099-4146
; Sequence 4146, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4146
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-4146

Query Match          97.1%; Score 34; DB 11; Length 482;
```


Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 94 GYWISAW 100

Db 103 GYWFAYW 109

Search completed: May 2, 2006, 09:33:44
Job time : 9.93023 secs

RESULT 14
US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens PfO-1
US-11-087-099-9097

Query Match 97.1%; Score 34; DB 11; Length 491;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 109 GYWISAW 115

RESULT 15
US-11-250-411-97
; Sequence 97, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 94.3%; Score 33; DB 11; Length 119;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 109 GYWISAW 115

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.2326 Seconds
(without alignments)
38.955 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	97.1	10	4 AAB99759	Aab99759 Rhesus D
2	34	97.1	12	4 AAB99769	Aab99769 Rhesus D
3	34	97.1	452	4 AAU03644	Aau03644 Group B S
4	34	97.1	466	6 ABU21589	Abu21589 Protein e
5	34	97.1	469	8 ADS44861	Ads44861 Bacterial
6	34	97.1	472	6 ABU38334	Abu38334 Protein e
7	34	97.1	474	6 ABU24881	Abu24881 Protein e
8	34	97.1	475	5 ABP30560	Abp30560 Streptoco
9	34	97.1	475	6 ABU40245	Abu40245 Protein e
10	34	97.1	475	6 ABU29756	Abu29756 Protein e
11	34	97.1	475	8 ADS24700	Ads24700 Bacterial
12	34	97.1	475	8 ADV87906	Adv87906 Streptoco
13	34	97.1	475	8 ADV81356	Adv81356 Streptoco
14	34	97.1	475	8 ADV79159	Adv79159 Streptoco
15	34	97.1	478	7 ADC97241	Adc97241 E. faeciu
16	34	97.1	479	5 ABP26968	Abp26968 Streptoco
17	34	97.1	490	5 ABB55389	Abb55389 Lactococc
18	34	97.1	496	5 ABB55385	Abb55385 Lactococc
19	34	97.1	499	7 ABO74582	Abu74582 Pseudomon
20	34	97.1	506	6 ABU22414	Abu22414 Protein e
21	34	97.1	585	7 ADA49403	Ada49403 Multi-epi
22	34	97.1	585	8 ADO24081	Ado24081 Epigene c
23	34	97.1	585	9 ADZ40583	Adz40583 HIV-TC mu
24	34	97.1	865	7 ABO70593	Abu70593 Pseudomon

25	33	94.3	10	5 ABP53931	Abp53931 VEGFR-3 b
26	33	94.3	10	5 ABP53932	Abp53932 VEGFR-3 b
27	33	94.3	69	4 AAO13595	Aao13595 Human pol
28	33	94.3	116	2 AAR15437	Aar15437 Heavy Cha
29	33	94.3	116	6 ABO27261	Abo27261 ICAM-1 bi
30	33	94.3	116	6 ABO27269	Abo27269 ICAM-1 bi
31	33	94.3	116	6 ABO27263	Abo27263 ICAM-1 bi
32	33	94.3	116	6 ABO27259	Abo27259 ICAM-1 bi
33	33	94.3	116	6 ABO27255	Abo27255 ICAM-1 bi
34	33	94.3	116	6 ABO27277	Abo27277 Humanised
35	33	94.3	116	6 ABO27273	Abo27273 Murine 1A
36	33	94.3	116	6 ABO27257	Abo27257 ICAM-1 bi
37	33	94.3	116	6 ABO27271	Abo27271 ICAM-1 bi
38	33	94.3	116	6 ABO27267	Abo27267 ICAM-1 bi
39	33	94.3	117	6 ABO27265	Abo27265 ICAM-1 bi
40	33	94.3	118	7 ADJ95639	Adj95639 Insulin-1
41	33	94.3	118	9 ADZ08201	Adz08201 IGF-speci
42	33	94.3	118	9 ADZ08173	Adz08173 IGF-speci
43	33	94.3	118	9 ADZ08158	Adz08158 IGF-speci
44	33	94.3	118	9 ADZ58532	Adz58532 VEGF rece
45	33	94.3	119	8 ADL11890	Adl11890 CDR trans

ALIGNMENTS

RESULT 1
AAB99759
ID AAB99759 standard; peptide; 10 AA.
XX
AC AAB99759;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rhesus D antibody binding peptide SEQ ID NO:4.
XX
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;
KW idiopathic thrombocytopenic purpura; immunoglobulin.
XX Homo sapiens.
XX
PN EP1106625-A1.
XX
PD 13-JUN-2001.
XX
PF 17-NOV-1999; 99EP-00122858.
XX
PR 17-NOV-1999; 99EP-00122858.
XX (ZLBB-) ZLB BIOPLASMA AG.
PI Miescher S, Hofmann A, Fisch I;
XX WPI; 2001-383568/41.
XX
PT Novel peptides capable of binding Rhesus D antibodies are used to
PT manufacture an agent for the diagnosis, therapy or prophylaxis of
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
PT newborn (HDN).
XX Claim 1; Page 12; 19pp; English.
PS
XX
CC The present sequence represents a peptide capable of binding Rhesus D
CC antibodies (I). Also described in the present invention are: (1) a
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
CC (II) operably linked to an expression control system; (3) a cell (IV)
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
CC peptides having immunologic properties of Rhesus D protein epitopes
CC comprising subjecting an antibody/antibody fragment recognising an
CC epitope of Rhesus D protein to several panning rounds with a phage
CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
CC manufacture an agent for the diagnosis, therapy or prophylaxis of
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
CC or removed from body fluids or immunoglobulin preparations. Using (I) as
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
CC with foreign erythrocytes thereby avoiding the risk of transmission of
CC viral diseases like AIDS and hepatitis B
XX
SQ Sequence 10 AA;

Query Match 97.1%; Score 34; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
| | | | |
Db 1 GYWSAKW 7

RESULT 2
AAB99769
ID AAB99769 standard; peptide; 12 AA.
XX
AC AAB99769;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rhesus D antibody related peptide #5.
XX
KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;
KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;
KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..12
XX
PN EP1106625-A1.
XX
PD 13-JUN-2001.
XX
PF 17-NOV-1999; 99EP-00122858.
XX
PR 17-NOV-1999; 99EP-00122858.
XX
PA (ZLBB-) ZLB BIOPLASMA AG.
XX
PI Miescher S, Hofmann A, Fisch I;
XX
DR WPI; 2001-383568/41.
XX
PT Novel peptides capable of binding Rhesus D antibodies are used to
PT manufacture an agent for the diagnosis, therapy or prophylaxis of
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
PT newborn (HDN).
XX
PS Example 1; Page 8; 19pp; English.
XX
CC The present invention describes peptides capable of binding Rhesus D
CC antibodies (I). Also described in the present invention are: (1) a
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more
CC (II) operably linked to an expression control system; (3) a cell (IV)
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)
CC peptides having immunologic properties of Rhesus D protein epitopes
CC comprising subjecting an antibody/antibody fragment recognising an
CC epitope of Rhesus D protein to several panning rounds with a phage

CC display library, and identifying immunogenic peptide sequences which are
CC mimotopes which differ in their amino acid sequence from the amino acid
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to
CC manufacture an agent for the diagnosis, therapy or prophylaxis of
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified
CC or removed from body fluids or immunoglobulin preparations. Using (I) as
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation
CC with foreign erythrocytes thereby avoiding the risk of transmission of
CC viral diseases like AIDS and hepatitis B. The present sequence represents
CC an anti-Rhesus D (RhD) antibody related peptide which is used in an
CC example from the present invention
XX
SQ Sequence 12 AA;

Query Match 97.1%; Score 34; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
| | | | |
Db 2 GYWSAKW 8

RESULT 3
AAU03644
ID AAU03644 standard; protein; 452 AA.
XX
AC AAU03644;
XX
DT 12-SEP-2001 (first entry)
XX
DE Group B Streptococcus antigenic protein, ID-119.
XX
KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
KW meningitis; neonate; antigenic; vaccine; infection; genital tract;
KW capsid polysaccharide vaccination.
XX
OS Streptococcus agalactiae.
XX
PN WO200132882-A2.
XX
PD 10-MAY-2001.
XX
PF 07-SEP-2000; 2000WO-GB003437.
XX
PR 07-SEP-1999; 99GB-00021125.
XX
PA (MICR-) MICROBIAL TECHNIKS LTD.
XX
PI Le Page RWF, Wells JM, Hanniffy SB;
XX
DR WPI; 2001-316444/33.
DR N-PSDB; AAS07061.
XX
PT New polypeptides derived from Streptococcus agalactiae are useful to
PT provide detection of, and vaccination against, Group B Streptococcus
PT infections, particularly to prevent infection in neonates.
XX
PS Claim 1; Fig 1; 178pp; English.
XX
CC AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
CC agalactiae) amino acid sequences of the invention. S. agalactiae is an
CC encapsulated bacterium which is a major pathogen of humans causing sepsis
CC and meningitis in neonates as well as adults. The S. agalactiae antigenic
CC polypeptides are used to vaccinate against Group B Streptococcus
CC infections, particularly to prevent infection in new born children
CC arising from the maternal genital tract. An immunogenic composition is
CC useful in the preparation of a medicament for the treatment or
CC prophylaxis of Group B Streptococcus infection. The invention does not
CC have the disadvantages of varied response rate associated with prior art

CC capsid polysaccharide vaccination against Group B Streptococcus
XX Sequence 452 AA;
SQ

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 92 GYWLSAW 98

RESULT 4
ABU21589
ID ABU21589 standard; protein; 466 AA.
XX
AC ABU21589;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by prokaryotic essential gene #7116.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Burkholderia fungorum.
OS
XX
XX WO200277183-A2.
PN
XX
PD 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX WPI; 2003-029926/02.
DR N-PSDB; ACA25459.
DR
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
PT
XX Claim 25; SEQ ID NO 49513; 1766pp; English.
PS
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 466 AA;
Query Match 97.1%; Score 34; DB 6; Length 466;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 86 GYWVSAW 92

RESULT 5
ADS44861
ID ADS44861 standard; protein; 469 AA.
XX
AC ADS44861;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23291.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
XX US2003233675-A1.
PN
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 23291; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 469 AA;

Query Match 97.1%; Score 34; DB 8; Length 469;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 97 GYWVASW 103

RESULT 6

ABU38334
ID ABU38334 standard; protein; 472 AA.

XX AC ABU38334;
XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #23861.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Pseudomonas aeruginosa.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA42204.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 66258; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 472 AA;

Query Match 97.1%; Score 34; DB 6; Length 472;

Best Local Similarity 57.1%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

||| |

Db 94 GYWISAW 100

RESULT 7

ABU24881

ID ABU24881 standard; protein; 474 AA.

XX AC ABU24881;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #10408.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Clostridium botulinum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA28751.

XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 52805; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 474 AA;

Query Match 97.1%; Score 34; DB 6; Length 474;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 95 GYWLAW 101

RESULT 8
ABP30560
ID ABP30560 standard; protein; 475 AA.
XX
AC ABP30560;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 10296.
XX
KW Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.
PR 07-MAR-2001; 2001GB-00005640.
XX
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
PI Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;
PI Tettelin H;
XX
DR WPI; 2002-352536/38.
DR N-PSDB; ABN71191.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 4161; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 5; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 92 GYWLAW 98

RESULT 9
ABU40245
ID ABU40245 standard; protein; 475 AA.
XX
AC ABU40245;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #25772.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Pseudomonas putida.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

```
PA (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA44115.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 68169; 1766pp; English.
PS
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 475 AA;
SQ
Query Match 97.1%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 93 GYWISAW 99
RESULT 10
ABU29756
ID ABU29756 standard; protein; 475 AA.
XX
XX ABU29756;
AC
XX 19-JUN-2003 (first entry)
DT
XX Protein encoded by Prokaryotic essential gene #15283.
DE
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW
XX Enterococcus faecium.
XX
XX WO200277183-A2.
PN
XX
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PD 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA33626.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
PS
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 475 AA;
SQ
Query Match 97.1%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 95 GYWLAW 101
RESULT 11
ADS24700
ID ADS24700 standard; protein; 475 AA.
XX
XX ADS24700;
AC
XX
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DT 02-DEC-2004 (first entry)
XX Bacterial polypeptide #13733.
DE
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 13733; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
DB 93 GYWISAW 99

RESULT 12
ADV87906
ID ADV87906 standard; protein; 475 AA.
XX
XX ADV87906;
AC
XX
DT 24-FEB-2005 (first entry)
XX
DE Streptococcus agalactiae protein sequence, SEQ ID 300.
XX
KW Antibacterial; Vaccine; bacterial infection.
XX
OS Streptococcus agalactiae.
XX
XX FR2824074-A1.
XX
XX 31-OCT-2002.
XX
XX 26-APR-2001; 2001FR-00005642.
XX
XX 26-APR-2001; 2001FR-00005642.
XX
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
XX
XX WPI; 2004-101891/11.
DR
XX
XX Genomic nucleotide sequences encoding polypeptides of Streptococcus
PT agalactiae for the development of vaccines, diagnostic tools, DNA chips
PT and identification of therapeutic targets.
XX
PS Claim 6; SEQ ID NO 300; 2687pp; French.
XX
CC The present invention relates to novel Streptococcus agalactiae
CC nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
CC agalactiae involved in the synthesis of amino acids, cell membranes, and
CC intermediate (central) metabolism, energetic metabolism, fatty acid, and
CC phospholipid metabolism, nucleotide metabolism including purines,
CC pyrimidines and/or nucleosides, regulatory functions, replication,
CC transcription, translation, protein transport, adaptation to atypical
CC conditions, sensitivity to medicines and/or analogues, functions related
CC to transporters, biosynthesis of cofactors, prosthetic groups and
CC transporters, cell membrane proteins and cellular machinery. (I) are
CC useful for the detection and/or amplification of nucleic acids.
CC Pharmaceutical composition comprising (I) or (II) are useful for
CC treatment of a bacterial S. agalactiae infection. Note: WO200292818A2 is
CC equivalent for the present basic patent FR2824074A1. WO200292818A2
CC contains 6617 sequence whereas the present patent only contains 2344
CC sequences.
XX
SQ Sequence 475 AA;

Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
DB 92 GYWLSAW 98

RESULT 13
ADV81356
ID ADV81356 standard; protein; 475 AA.
XX
XX ADV81356;
AC
XX
DT 24-FEB-2005 (first entry)

XX Streptococcus agalactiae protein, SEQ ID 2497.
DE Antibacterial; vaccine; bacterial infection.
XX Streptococcus agalactiae.
KW WO200292818-A2.
XX 21-NOV-2002.
OS 26-APR-2002; 2002WO-IB003059.
PN 26-APR-2001; 2001FR-00005642.
XX (INSP) INST PASTEUR.
PD (CNRS) CNRS CENT NAT RECH SCI.
XX Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX WPI; 2004-101891/11.
DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX and identification of therapeutic targets.
PS Claim 6; SEQ ID NO 2497; 439pp; French.
XX The present invention relates to novel Streptococcus agalactiae
CC nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
CC novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
CC nucleotide sequences encode polypeptides of S. agalactiae involved in the
CC synthesis of amino acids, cell membranes, intermediate (central)
CC metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
CC nucleotide metabolism including purines, pyrimidines and/or nucleosides,
CC regulatory functions, replication, transcription, translation, protein
CC transport, adaptation to atypical conditions, sensitivity to medicines
CC and/or analogues, functions related to transposons, biosynthesis of
CC cofactors, prosthetic groups and transporters, cell membrane proteins and
CC cellular machinery. (I) are useful for the detection and/or amplification
CC of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
CC useful for treatment of a bacterial S. agalactiae infection. The complete
CC genome of Streptococcus agalactiae is given in ADV81204. Note: The
CC present patent is an equivalent for the basic patent FR2824074A1, which
CC contains only 2344 sequences.
XX
SQ Sequence 475 AA;
Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 92 GYWLSAW 98
RESULT 14
ADV79159
ID ADV79159 standard; protein; 475 AA.
XX
AC ADV79159;
XX 24-FEB-2005 (first entry)
XX Streptococcus agalactiae protein, SEQ ID 300.
DE Antibacterial; vaccine; bacterial infection.
KW Streptococcus agalactiae.
XX
OS
XX WO200292818-A2.
PN

XX 21-NOV-2002.
XX 26-APR-2002; 2002WO-IB003059.
PF 26-APR-2001; 2001FR-00005642.
XX (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
PI Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX WPI; 2004-101891/11.
DR Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX and identification of therapeutic targets.
PS Claim 6; SEQ ID NO 300; 439pp; French.
XX The present invention relates to novel Streptococcus agalactiae
CC nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
CC novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
CC nucleotide sequences encode polypeptides of S. agalactiae involved in the
CC synthesis of amino acids, cell membranes, intermediate (central)
CC metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
CC nucleotide metabolism including purines, pyrimidines and/or nucleosides,
CC regulatory functions, replication, transcription, translation, protein
CC transport, adaptation to atypical conditions, sensitivity to medicines
CC and/or analogues, functions related to transposons, biosynthesis of
CC cofactors, prosthetic groups and transporters, cell membrane proteins and
CC cellular machinery. (I) are useful for the detection and/or amplification
CC of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
CC useful for treatment of a bacterial S. agalactiae infection. The complete
CC genome of Streptococcus agalactiae is given in ADV81204. Note: The
CC present patent is an equivalent for the basic patent FR2824074A1, which
CC contains only 2344 sequences.
XX
SQ Sequence 475 AA;
Query Match 97.1%; Score 34; DB 8; Length 475;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 92 GYWLSAW 98
RESULT 15
ADC97241
ID ADC97241 standard; protein; 478 AA.
XX
AC ADC97241;
XX 01-JAN-2004 (first entry)
DT
XX
DE E. faecium protein sequence SEQ ID 6868.
XX
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX Enterococcus faecium.
OS
XX US6583275-B1.
PN
XX 24-JUN-2003.
PD
XX 30-JUN-1998; 98US-00107532.
PF
XX 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
PR

XX (GENO-) GENOME THERAPEUTICS CORP.
PA Doucette-Stamm LA, Bush D;
XX
XX
XX
DR WPI; 2003-799836/75.
DR N-PSDB; ADC93587.
XX
PT New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
PS Example 1; SEQ ID NO 6868; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX
SQ Sequence 478 AA;

Query Match 97.1%; Score 34; DB 7; Length 478;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
 |||
Db 98 GYWLSAW 104

Search completed: May 2, 2006, 08:54:54
Job time : 93.2326 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:47:12 ; Search time 14.5116 Seconds
(without alignments)
53.043 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	72	2 T03190	hypothetical prote
2	34	97.1	108	2 S12193	hypothetical prote
3	34	97.1	345	2 T37139	hypothetical prote
4	34	97.1	469	2 D70048	ABC transporter (a
5	34	97.1	472	2 E83497	probable amino aci
6	34	97.1	475	2 T46745	arginine/ornithine
7	34	97.1	482	2 JH0110	arginine/ornithine
8	34	97.1	490	2 C86879	arginine/ornithine
9	34	97.1	497	2 G86878	ig heavy chain pre
10	33	94.3	142	2 C34903	CDPdiacylglycerol-
11	33	94.3	227	2 S73905	hypothetical prote
12	33	94.3	250	2 A69843	oligopeptide ABC t
13	33	94.3	289	2 G72215	hypothetical prote
14	33	94.3	360	2 AE2047	hypothetical prote
15	33	94.3	441	2 C95307	probable transport
16	33	94.3	508	2 C95282	probable ABC trans
17	33	94.3	517	2 A13201	hypothetical prote
18	33	94.3	519	2 E83268	probable carbohydr
19	33	94.3	534	2 T15414	hypothetical prote
20	33	94.3	535	2 B95952	probable dipeptide
21	33	94.3	541	2 AC2392	hypothetical prote
22	33	94.3	563	2 AH2975	hypothetical prote
23	33	94.3	563	2 C98307	opha protein limpo
24	33	94.3	592	2 T15413	hypothetical prote
25	33	94.3	778	2 T31037	hypothetical prote
26	33	94.3	1502	2 T42216	multidrug resistan
27	32	91.4	71	2 S22905	lysis protein S -
28	32	91.4	83	2 E69903	hypothetical prote
29	32	91.4	187	2 G83047	hypothetical prote

30	32	91.4	218	2	S76385	hypothetical prote
31	32	91.4	218	2	D87264	hypothetical prote
32	32	91.4	257	2	E75325	probable mccf prot
33	32	91.4	261	2	JC5806	aquaporin 8 - mous
34	32	91.4	263	2	JC5622	aquaporin 8 - rat
35	32	91.4	271	2	F83188	phosphatidate cyti
36	32	91.4	271	2	JC4832	phosphatidate cyti
37	32	91.4	282	2	H95869	probable sugar ABC
38	32	91.4	286	2	E88690	protein F41H10.7 [
39	32	91.4	344	2	C82611	hypothetical prote
40	32	91.4	447	2	H97146	siderophore/Surfac
41	32	91.4	448	2	AB0301	conserved hypothet
42	32	91.4	466	2	T35164	probable secreted
43	32	91.4	519	2	S77572	oligopeptide trans
44	32	91.4	536	2	G95389	probable ABC trans
45	32	91.4	631	2	B86233	hypothetical prote

ALIGNMENTS

RESULT 1
T03190
hypothetical protein 72B - rice mitochondrion
C;Species: mitochondrion Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03190
R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existel
A;Reference number: Z14841; MUID:95211382; PMID:7545979
A;Accession: T03190
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <ITA>
A;Cross-references: UNIPROT:Q35302; UNIPARC:UPI000009746F; EMBL:D32052; NID:G769704; P
A;Experimental source: cultivar Nipponbare
C;Genetics:
A;Genome: mitochondrion
C;Keywords: mitochondrion

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	GYWXXXW	7
Db	34	GYWSSHW	40

RESULT 2
S12193
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1
C;Species: Thiobacillus ferrooxidans
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S12193
R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidan
A;Reference number: S12188; MUID:91125140; PMID:2280689
A;Accession: S12193
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <DRO>
A;Cross-references: UNIPROT:P20088; UNIPARC:UPI000013B9EC; EMBL:X52699; NID:G48158; P
C;Genetics:
A;Genome: plasmid pTF1

Query Match 97.1%; Score 34; DB 2; Length 108;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	GYWXXXW	7
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Db      89 GYWRSSW 95

RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37139
R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <HAR>
A;Cross-references: UNIPROT:Q9S1R7; UNIPARC:UPI00000DB3A4; EMBL:AL109972; PIDN:CAB53264.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ9A.03c
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: D70048
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallego; J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois; A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron; akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D70048
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KUN>
A;Cross-references: UNIPROT:O32204; UNIPARC:UPI0000060A54; GB:Z99121; GB:AL009126; NID:9
A;Experimental source: strain 168
C;Genetics:
A;Gene: yvsh
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      97 GYWVASW 103

RESULT 5
E83497
probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Eadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
A;Cross-references: UNIPROT:Q9I4E4; UNIPARC:UPI00000C529E; GB:AE004549; GB:AE004091; NID:9
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1194
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      94 GYWISAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: T46745
R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of the arginine/ornithine antiporter.
A;Reference number: Z23141; MUID:98361904; PMID:9696763
A;Accession: T46745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Cross-references: UNIPROT:O53092; UNIPARC:UPI0000125DAC; EMBL:AJ001330; NID:92764610;
C;Genetics:
A;Gene: arcD
C;Function:
A;Description: necessary for arginine transport; involved in ornithine-arginine exchange
A;Pathway: arginine catabolism
C;Superfamily: ecotropic retrovirus receptor protein

Query Match      97.1%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      94 GYWLSAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004
C;Accession: JH0110; A82999
R;Luethi, E.; Baur, H.; Gamper, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D. Gene 87, 37-43, 1990
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cor
A;Reference number: JH0110; MUID:90236296; PMID:2158926
A;Accession: JH0110
```


A;Molecule type: DNA
A;Residues: 1-482 <LUE>
A;Cross-references: UNIPROT:P18275; UNIPARC:UPI00000618AA; GB:M33223; NID:G151030; PIDN:
A;Experimental source: strain PA01
A;Note: the gene encoding this protein is located upstream of the arcABC genes which end
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A82999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <STO>
A;Cross-references: UNIPARC:UPI00000618AA; GB:AE004930; NID:G9951472; PIDN:
A;Experimental source: strain PA01
C;Genetics:
A;Gene: arcD; PA5170
C;Superfamily: ecotropic retrovirus receptor protein
C;Keywords: transmembrane protein

Query Match 97.1%; Score 34; DB 2; Length 482;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 94 GYWISAW 100

RESULT 8
C86879
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C;Accession: C86879
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <STO>
A;Cross-references: UNIPROT:Q9CE15; UNIPARC:UPI000006B99; GB:AE005176; PID:G12725084; F
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcD1
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 490;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 93 GYWLAW 99

RESULT 9
G86878
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004
C;Accession: G86878
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86878
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-497 <STO>
A;Cross-references: UNIPROT:Q9CE19; UNIPARC:UPI000006B95; GB:AE005176; PID:G12725079;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcD2
C;Superfamily: ecotropic retrovirus receptor protein

Query Match 97.1%; Score 34; DB 2; Length 497;
Best Local Similarity 57.1%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 93 GYWISAW 99

RESULT 10
C34903
Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C;Accession: C34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-r
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
A;Cross-references: UNIPARC:UPI0000176C0F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 94.3%; Score 33; DB 2; Length 142;
Best Local Similarity 57.1%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 126 GYWFAYW 132

RESULT 11
S73905
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgSA - M
N;Alternate names: hypothetical protein A65_orf227
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S73905
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73905
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-227 <HIM>
A;Cross-references: UNIPROT:P75520; UNIPARC:UPI0000131886; EMBL:AE000057; GB:U00089; N
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: pgSA
A;Genetic code: SGC3
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C;Keywords: transferase

Query Match 94.3%; Score 33; DB 2; Length 227;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 84 GYWARKW.90

RESULT 12

A69843

hypothetical protein yjba - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: A69843

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: A69843

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-250 <KUN>

A;Cross-references: UNIPROT:O31597; UNIPARC:UPI0000060207; GB:Z99110; GB:AL009126; NID:9

A;Experimental source: strain 168

C;Genetics:

A;Gene: yjba

C;Superfamily: Bacillus subtilis hypothetical protein yjba

Query Match 94.3%; Score 33; DB 2; Length 250;

Best Local Similarity 57.1%; Pred. No. 66;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 185 GYWTW 191

RESULT 13

G72215

oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: G72215

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: G72215

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-289 <ARN>

A;Cross-references: UNIPROT:Q9X270; UNIPARC:UPI00000D385E; GB:AE001813; GB:AE000512; NID

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1748

C;Superfamily: oligopeptide permease protein oppB

Query Match 94.3%; Score 33; DB 2; Length 289;

Best Local Similarity 57.1%; Pred. No. 75;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 11 GYWKAFW 17

RESULT 14

AE2047

hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AE2047

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2047

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-360 <KUR>

A;Cross-references: UNIPROT:Q8YVP3; UNIPARC:UPI00000CE269; GB:BA000019; PIDN:BA073630.1

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all1931

Query Match 94.3%; Score 33; DB 2; Length 360;

Best Local Similarity 57.1%; Pred. No. 91;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 127 GYWSYGW 133

RESULT 15

C95307

probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) me

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 05-Oct-2004

C;Accession: C95307

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bov ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: C95307

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-441 <KUR>

A;Cross-references: UNIPROT:Q922T6; UNIPARC:UPI00000CB08F; GB:AE006469; PIDN:AAK65021.1

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, i

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Sma0684

A;Genome: plasmid

C;Superfamily: ecotropic retrovirus receptor protein

Query Match 94.3%; Score 33; DB 2; Length 441;

Best Local Similarity 57.1%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7

Db 92 GYWISIW 98

us-10-046-922-68.rpr

Tue May 2 12:32:43 2006

Search completed: May 2, 2006, 08:56:18
Job time : 17.5116 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:38:27 ; Search time 90.6047 Seconds
(without alignments)
62.295 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	72	Q35302 ORYSA	Q35302 oryza sativ
2	34	97.1	108	YML2 THIFE	P20088 thioabacillu
3	34	97.1	130	Q7U395 PROMP	Q7u395 prochloroco
4	34	97.1	236	Q9WGW9_9HIV1	Q9w9 human immun
5	34	97.1	253	Q32816_LACLC	Q32816 lactococcus
6	34	97.1	294	Q8ET30_OCEIH	Q8et30 oceanobacil
7	34	97.1	333	Q6F6U4_ACIAD	Q6f6u4 acinetobact
8	34	97.1	345	Q9S1R7_STRCO	Q9s1r7 streptomyce
9	34	97.1	451	Q62C74_BURMA	Q62c74 burkholderi
10	34	97.1	459	Q9KGV3_LACLA	Q9kgv3 lactococcus
11	34	97.1	464	Q84DL5_OENOE	Q84dl5 oenococcus
12	34	97.1	465	Q6I3F7_BACAN	Q6i3f7 bacillus an
13	34	97.1	465	Q4MN56_BACCE	Q4mn56 bacillus ce
14	34	97.1	465	Q81H27_BACCR	Q81hz7 bacillus ce
15	34	97.1	465	Q63G16_BACCR	Q63g16 bacillus ce
16	34	97.1	465	Q6HNI4_BACHK	Q6hni4 bacillus th
17	34	97.1	465	Q73DL5_BACCI	Q73dl5 bacillus ce
18	34	97.1	465	Q81V71_BACAN	Q81v71 bacillus an
19	34	97.1	467	Q65F15_BACLD	Q65f15 bacillus li
20	34	97.1	469	Q6TK71_STRRT	Q6tk71 streptococc
21	34	97.1	469	Q32204_BACSU	Q32204 bacillus su
22	34	97.1	471	Q6HP27_BACHK	Q6hp27 bacillus th
23	34	97.1	471	Q73E85_BACCI	Q73e85 bacillus ce
24	34	97.1	471	Q81IH9_BACCR	Q81ih9 bacillus ce
25	34	97.1	472	Q9I4E4_PSEAE	Q9i4e4 pseudomonas
26	34	97.1	473	Q7NRJ8_CHRVO	Q7nrj8 chromobacte
27	34	97.1	475	1 ARCD_LACSK	Q53092 lactobacill
28	34	97.1	475	Q4ZT00_PSESY	Q4zt00 pseudomonas
29	34	97.1	475	Q4K7R6_PSEF5	Q4k7r6 pseudomonas
30	34	97.1	475	Q4K7R5_PSEF5	Q4k7r5 pseudomonas
31	34	97.1	475	2 Q88P50_PSEPK	Q88p50 pseudomonas

32	34	97.1	475	2	Q88P51_PSEPK	Q88p51 pseudomonas
33	34	97.1	475	2	Q8DWP9_STRAS	Q8dwp9 streptococc
34	34	97.1	475	2	Q8E2J7_STRAS	Q8e2j7 streptococc
35	34	97.1	478	1	ARCD_CLOPE	Q46170 clostridium
36	34	97.1	482	1	ARCD_PSEAE	P18275 pseudomonas
37	34	97.1	486	2	Q63U74_BURPS	Q63u74 burkholderi
38	34	97.1	486	2	Q62KE0_BURMA	Q62ke0 burkholderi
39	34	97.1	490	2	Q9CE15_LACLA	Q9ce15 lactococcus
40	34	97.1	496	2	Q63L96_BURPS	Q63l96 burkholderi
41	34	97.1	497	2	Q9KGV0_LACLA	Q9kgv0 lactococcus
42	34	97.1	497	2	Q9CE19_LACLA	Q9ce19 lactococcus
43	34	97.1	526	2	Q9K574_9LACT	Q9k574 lactococcus
44	34	97.1	552	2	Q5LSW7_SILPO	Q5ls7 silicibacte
45	34	97.1	753	2	Q4TSN3_9SPHN	Q4tsn3 erythrobact

ALIGNMENTS

RESULT 1
Q35302 ORYSA
ID Q35302_ORYSA PRELIMINARY; PRT; 72 AA.
AC Q35302;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE ORF72B.

OS Oryza sativa (japonica cultivar-group).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,
RA Il'in Y.V.;
RT "Structure of long and short copies of the mobile dispersed gene MDG3
of Drosophila melanogaster.";
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95308541; PubMed=7788722; DOI=10.1007/BF00313433;
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiura M.,
RA Hirai A.;
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is
transcribed from alternative promoters.";
RL Curr. Genet. 27:184-189(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95211382; PubMed=7545979;
RA Itadani H., Wakasugi T., Sugita M., Sugiura M., Nakazono M., Hirai A.;
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
RL Plant Cell Physiol. 35:1239-1244(1994).
DR EMBL; D32052; BAA06811.1; -; Genomic_DNA.
DR PIR; T03190; T03190.
DR Gramene; Q35302; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 97.1%; Score 34; DB 2; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 34 GYWSSHW 40

RESULT 2

YML2_THIFE
ID_YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3'region (ORF 4).
OS Thiobacillus ferrooxidans.
OG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
RT ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X52699; CAA36930.1; -; Genomic_DNA.
DR PIR; S12193; S12193.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 97.1%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 89 GYWRSSW 95

RESULT 3
Q7U395_PROMP PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf).
GN OrderedLocusNames=PMW1067;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19526.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 7 GYWT LAW 13

RESULT 4
Q9WGW9_9HIV1 PRELIMINARY; PRT; 236 AA.
AC Q9WGW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:
RT the ariel project for the prevention of transmission of HIV from
RT mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -; Genomic_DNA.
DR HSSP; P03366; 1HRH.
DR SMR; Q9WGW9; 1-236.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PS50879; RNase_H; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 129 GYWQATW 135

RESULT 5
O32816_LACLC PRELIMINARY; PRT; 253 AA.
AC O32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).

```
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MG1363;
RX MEDLINE=97369814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
RT by ISS1 transposition.";
RL J. Bacteriol. 179:4473-4479(1997).
DR EMBL; U81991; AAC45504.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR02293; AA/rel_permease.
KW Transmembrane.
FT NON_TER 253
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||
Db 93 GYWLAW 99

RESULT 6
Q8ET30_OCEIH PRELIMINARY; PRT; 294 AA.
AC Q8ET30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter permease.
GN OrderedLocusNames=OB0434;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC12390.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR InterPro; IPR001626; ABC_3.
DR Pfam; PF00950; ABC-3; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;

Query Match 97.1%; Score 34; DB 2; Length 294;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||
Db 244 GYWIATW 250

RESULT 7
Q6F6U4_ACIAAD PRELIMINARY; PRT; 333 AA.
ID Q6F6U4_ACIAAD PRELIMINARY;
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AC Q6F6U4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transporter; putative sodium/bile acid transporter family
DE protein.
GN OrderedLocusNames=ACIAD3583;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP1;
RX PubMed=15514110; DOI=10.1093/nar/gkh910;
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CRS43861; CAG70223.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008508; F:bile acid:sodium symporter activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR002657; BilAc/Na_symport.
DR Pfam; PF01758; SBF; 1.
KW Complete proteome.
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 333;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
   |||
Db 252 GYWASRW 258

RESULT 8
Q9SLR7_STRCO PRELIMINARY; PRT; 345 AA.
AC Q9SLR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCO0224.
GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939104; CAB53264.1; -; Genomic_DNA.
DR PIR; T37139; T37139.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;
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Query Match          97.1%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 147 GYWAARW 153

RESULT 9
Q62C74 BURMA
ID Q62C74 BURMA PRELIMINARY; PRT; 451 AA.
AC Q62C74;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Amino acid permease.
GN OrderedLocusNames=BMAA1038;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Niernan W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammad Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000011; AAU46467.1; -; Genomic_DNA.
DR TIGR; BMAA1038; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Complete proteome.
KW SEQUENCE 451 AA; 47344 MW; ED2D1ADDEB0C4A55 CRC64;
SQ

Query Match          97.1%; Score 34; DB 2; Length 451;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 116 GYVWSAW 122

RESULT 10
Q9KGV3 LACLA
ID Q9KGV3 LACLA PRELIMINARY; PRT; 459 AA.
AC Q9KGV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ArcD1.
GN Name=arcD1;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ML3;
RA Chou L., Weimer B., Xie Y.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL
```

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[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ML3;
RC Chou L.-S., Weimer B., Xie Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282249; AAF86987.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Transmembrane; Transport.
KW SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;
SQ

Query Match          97.1%; Score 34; DB 2; Length 459;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 92 GYWLAW 98

RESULT 11
Q84DL5 OENOE
ID Q84DL5 OENOE PRELIMINARY; PRT; 464 AA.
AC Q84DL5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arginine/ornithine antiporter ArcD2.
GN Name=arcD2;
OS Oenococcus oeni (Leuconostoc oenos).
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.
OX NCBI_TaxID=1247;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23279;
RX MEDLINE=22519090; PubMed=12631210;
RX DOI=10.1046/j.1365-2672.2003.01907.x;
RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;
RT "Molecular characterization of Oenococcus oeni genes encoding proteins involved in arginine transport.";
RL J. Appl. Microbiol. 94:738-746(2003).
DR EMBL; AF541253; AA083382.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
DR Transmembrane; Transport.
KW SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;
SQ

Query Match          97.1%; Score 34; DB 2; Length 464;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 94 GYWLSSW 100

RESULT 12
Q6I3F7 BACAN
ID Q6I3F7 BACAN PRELIMINARY; PRT; 465 AA.
AC Q6I3F7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BAS0596;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017225; AAT52924.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

RESULT 13
Q4MN56 BACCE PRELIMINARY; PRT; 465 AA.
ID Q4MN56 BACCE PRELIMINARY;
AC Q4MN56;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Arginine/ornithine antiporter.
GN Name=arcD; ORFNames=BCE_G9241_0606;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAEK0100024; EAL13575.1; -; Genomic DNA.
SQ SEQUENCE 465 AA; 50180 MW; F2A1540B055C90B9 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

RESULT 14
Q81HZ7 BACCR PRELIMINARY; PRT; 465 AA.
ID Q81HZ7 BACCR PRELIMINARY;
AC Q81HZ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Arginine/ornithine antiporter.
GN OrderedLocusNames=BC0629;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017000; AAP07646.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome.
SQ SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

RESULT 15
Q63G16 BACCZ PRELIMINARY; PRT; 465 AA.
ID Q63G16 BACCZ PRELIMINARY;
AC Q63G16;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable arginine/ornithine antiporter protein.
GN Name=arcD;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU19700.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50178 MW; 55D7083AAE7B3958 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 96 GYWAANW 102

Search completed: May 2, 2006, 08:46:43
Job time : 93.6047 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 08:55:22 ; Search time 22.6977 Seconds
(without alignments)
29.140 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	97.1	478	US-09-107-532A-6868	Sequence 6868, Ap
2	34	97.1	499	US-09-252-991A-23328	Sequence 23328, A
3	34	97.1	865	US-09-252-991A-19339	Sequence 19339, A
4	33	94.3	543	US-09-252-991A-18697	Sequence 18697, A
5	33	94.3	1498	US-09-792-616-9	Sequence 9, Appli
6	33	94.3	1503	US-09-792-616-3	Sequence 3, Appli
7	33	94.3	1503	US-09-647-140B-8	Sequence 8, Appli
8	32	91.4	88	US-09-902-540-12675	Sequence 12675, A
9	32	91.4	177	US-09-543-681A-7620	Sequence 7620, Ap
10	32	91.4	252	US-09-502-653-10	Sequence 10, Appl
11	32	91.4	263	US-09-610-906-12	Sequence 12, Appl
12	32	91.4	274	US-09-248-796A-15791	Sequence 15791, A
13	32	91.4	278	US-09-145-828A-11	Sequence 11, Appl
14	32	91.4	278	US-09-903-456-18	Sequence 18, Appl
15	32	91.4	278	US-09-624-670-17	Sequence 17, Appl
16	32	91.4	339	US-09-252-991A-26841	Sequence 26841, A
17	32	91.4	362	US-08-415-751-6	Sequence 6, Appli
18	32	91.4	367	US-09-248-796A-15188	Sequence 15188, A
19	32	91.4	492	US-09-107-532A-6945	Sequence 6945, Ap
20	32	91.4	500	US-09-252-991A-21214	Sequence 21214, A
21	31	88.6	185	US-10-808-807-12	Sequence 12, Appl
22	31	88.6	342	US-09-252-991A-32031	Sequence 32031, A
23	30	85.7	11	US-09-069-827A-87	Sequence 87, Appl
24	30	85.7	16	US-09-620-091-81	Sequence 81, Appl
25	30	85.7	519	US-09-198-452A-479	Sequence 479, App
26	30	85.7	519	US-09-438-185A-454	Sequence 454, App
27	30	85.7	654	US-09-252-991A-18441	Sequence 18441, A

28	30	85.7	2357	2	US-09-949-016-9656	Sequence 9656, Ap
29	29	82.9	26	2	US-09-962-756-1516	Sequence 1516, Ap
30	29	82.9	34	2	US-09-270-767-60715	Sequence 60715, A
31	29	82.9	35	2	US-09-082-279B-1191	Sequence 1191, Ap
32	29	82.9	35	2	US-09-315-304B-1191	Sequence 1191, Ap
33	29	82.9	35	2	US-09-834-784-1191	Sequence 1191, Ap
34	29	82.9	35	2	US-09-515-965A-1191	Sequence 1191, Ap
35	29	82.9	35	2	US-09-350-641C-1191	Sequence 1191, Ap
36	29	82.9	35	2	US-09-350-841A-1191	Sequence 1191, Ap
37	29	82.9	55	2	US-09-621-976-7633	Sequence 7633, Ap
38	29	82.9	69	2	US-09-621-976-7239	Sequence 7239, Ap
39	29	82.9	139	2	US-09-252-991A-19685	Sequence 19685, A
40	29	82.9	142	2	US-09-252-991A-22994	Sequence 22994, A
41	29	82.9	197	2	US-09-543-681A-5312	Sequence 5312, Ap
42	29	82.9	227	2	US-09-489-039A-8752	Sequence 8752, Ap
43	29	82.9	255	2	US-09-270-767-45223	Sequence 45223, A
44	29	82.9	286	2	US-09-712-363-168	Sequence 168, Appl
45	29	82.9	291	2	US-10-272-490-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-107-532A-6868
; Sequence 6868, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6868:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868

Query Match 97.1%; Score 34; DB 2; Length 478;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 98 GYWLSAW 104

RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match 97.1%; Score 34; DB 2; Length 499;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 111 GYWISAW 117

RESULT 3
US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19339
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19339

Query Match 97.1%; Score 34; DB 2; Length 865;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 487 GYWISAW 493

RESULT 4

US-09-252-991A-18697
; Sequence 18697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18697
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697

Query Match 94.3%; Score 33; DB 2; Length 543;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 331 GYWMVSW 337

RESULT 5
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match 94.3%; Score 33; DB 2; Length 1498;
Best Local Similarity 57.1%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 960 GYWLSLW 966

RESULT 6
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	1 GYWXXXW 7 		
Db	210 GYWEPAW 216		
RESULT 11			
US-09-610-906-12			
; Sequence 12, Application US/09610906			
; Patent No. 6566066			
; GENERAL INFORMATION:			
; APPLICANT: Walker, Michael G.			
; APPLICANT: Volkmut, Wayne			
; APPLICANT: Klingner, Tod M.			
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT			
; FILE REFERENCE: PC-0012 CIP			
; CURRENT APPLICATION NUMBER: US/09/610,906			
; CURRENT FILING DATE: 2000-07-06			
; PRIOR APPLICATION NUMBER: 09/226,994			
; PRIOR FILING DATE: 1999-01-07			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PERL Program			
; SEQ ID NO 12			
; LENGTH: 263			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: GenBank ID No. 6566066: G2346968			
; PUBLICATION INFORMATION:			
US-09-610-906-12			
Query Match 91.4%; Score 32; DB 2; Length 263;			
Best Local Similarity 57.1%; Pred. No. 2.4e+02;			
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	1 GYWXXXW 7 		
Db	224 GYWDFHW 230		
RESULT 12			
US-09-248-796A-15791			
; Sequence 15791, Application US/09248796A			
; Patent No. 6747137			
; GENERAL INFORMATION:			
; APPLICANT: Keith Weinstock et al			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN			
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: 107196.132			
; CURRENT APPLICATION NUMBER: US/09/248,796A			
; CURRENT FILING DATE: 1999-02-12			
; PRIOR APPLICATION NUMBER: US 60/074,725			
; PRIOR FILING DATE: 1998-02-13			
; PRIOR APPLICATION NUMBER: US 60/096,409			
; PRIOR FILING DATE: 1998-08-13			
; NUMBER OF SEQ ID NOS: 28208			
; SEQ ID NO 15791			
; LENGTH: 274			
; TYPE: PRT			
; ORGANISM: Candida albicans			
US-09-248-796A-15791			
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Best Local Similarity 57.1%; Pred. No. 2.5e+02;			
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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Db	84 GYWPITW 90		

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	1 GYWXXXW 7 		
Db	108 GYWIFLW 114		
RESULT 13			
US-09-145-828A-11			
; Sequence 11, Application US/09145828A			
; Patent No. 6403349			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Mukerji, Pradip			
; APPLICANT: Leonard, Amanda E. Y.			
; APPLICANT: Huang, Yung-Sheng			
; APPLICANT: Thurmond, Jennifer J.			
; APPLICANT: Kirchner, Stephen J.			
; APPLICANT: Parker-Barnes, Jennifer M.			
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF			
; FILE REFERENCE: 6407.US.O1			
; CURRENT APPLICATION NUMBER: US/09/145,828A			
; CURRENT FILING DATE: 1998-09-02			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 11			
; LENGTH: 278			
; TYPE: PRT			
; ORGANISM: Caenorhabditis elegans			
US-09-145-828A-11			
Query Match 91.4%; Score 32; DB 2; Length 278;			
Best Local Similarity 57.1%; Pred. No. 2.5e+02;			
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	1 GYWXXXW 7 		
Db	108 GYWIFLW 114		
RESULT 14			
US-09-903-456-18			
; Sequence 18, Application US/09903456			
; Patent No. 6677145			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Mukerji, Pradip			
; APPLICANT: Leonard, Amanda Eun-Yeong			
; APPLICANT: Huang, Yung-Sheng			
; APPLICANT: Pereira, Suzette L.			
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF			
; FILE REFERENCE: 6407.US.P3			
; CURRENT APPLICATION NUMBER: US/09/903,456			
; CURRENT FILING DATE: 2001-07-11			
; PRIOR APPLICATION NUMBER: US 09/624,670			
; PRIOR FILING DATE: 2000-07-24			
; PRIOR APPLICATION NUMBER: US 09/379,095			
; PRIOR FILING DATE: 1999-08-23			
; PRIOR APPLICATION NUMBER: US 09/145,828			
; PRIOR FILING DATE: 1998-09-02			
; NUMBER OF SEQ ID NOS: 116			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 18			
; LENGTH: 278			
; TYPE: PRT			
; ORGANISM: Caenorhabditis elegans			
US-09-903-456-18			
Query Match 91.4%; Score 32; DB 2; Length 278;			
Best Local Similarity 57.1%; Pred. No. 2.5e+02;			
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	1 GYWXXXW 7 		
Db	108 GYWIFLW 114		
RESULT 15			
US-09-624-670-17			
; Sequence 17, Application US/09624670			

Patent No. 6913916
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Das, Tapas
APPLICANT: Huang, Yung-Sheng
APPLICANT: Parker-Barnes, Jennifer M.
APPLICANT: Leonard, Amanda Eun-yeong
APPLICANT: Thurmond, Jennifer M.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P2
CURRENT APPLICATION NUMBER: US/09/624,670
CURRENT FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 278
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-624-670-17

Query Match 91.4%; Score 32; DB 2; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7
Db 108 GYWIFLW 114

Search completed: May 2, 2006, 08:58:25
Job time : 23.6977 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: May 2, 2006, 09:23:40 ; Search time 74.4186 Seconds
(without alignments)
44.917 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXXXWX 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	58	4	US-10-425-115-308836 Sequence 308836,
2	34	97.1	72	4	US-10-437-963-176036 Sequence 176036,
3	34	97.1	452	4	US-10-091-007-88 Sequence 88, Appl
4	34	97.1	466	4	US-10-282-122A-49513 Sequence 49513, A
5	34	97.1	469	4	US-10-369-493-23291 Sequence 23291, A
6	34	97.1	472	4	US-10-282-122A-66258 Sequence 66258, A
7	34	97.1	474	4	US-10-282-122A-52805 Sequence 52805, A
8	34	97.1	475	4	US-10-369-493-13733 Sequence 13733, A
9	34	97.1	475	4	US-10-282-122A-57680 Sequence 57680, A
10	34	97.1	475	4	US-10-282-122A-68169 Sequence 68169, A
11	34	97.1	506	4	US-10-282-122A-50338 Sequence 50338, A
12	34	97.1	585	3	US-09-894-018-87 Sequence 87, Appl
13	34	97.1	585	5	US-10-474-960A-87 Sequence 34, Appl
14	33	94.3	10	4	US-10-046-922-34 Sequence 34, Appl
15	33	94.3	10	4	US-10-046-922-35 Sequence 35, Appl
16	33	94.3	47	4	US-10-425-115-287762 Sequence 287762,
17	33	94.3	104	4	US-10-425-115-273234 Sequence 273234,
18	33	94.3	116	3	US-09-910-483-1 Sequence 1, Appli
19	33	94.3	116	3	US-09-910-483-5 Sequence 5, Appli
20	33	94.3	116	3	US-09-910-483-9 Sequence 9, Appli
21	33	94.3	116	3	US-09-910-483-13 Sequence 13, Appl
22	33	94.3	116	3	US-09-910-483-17 Sequence 17, Appl
23	33	94.3	116	3	US-09-910-483-21 Sequence 21, Appl
24	33	94.3	116	3	US-09-910-483-25 Sequence 25, Appl
25	33	94.3	116	3	US-09-910-483-29 Sequence 29, Appl
26	33	94.3	116	3	US-09-910-483-33 Sequence 33, Appl
27	33	94.3	116	3	US-09-910-483-37 Sequence 37, Appl

28	33	94.3	116	3	US-09-910-483-41	Sequence 41, Appl
29	33	94.3	116	3	US-09-910-483-43	Sequence 43, Appl
30	33	94.3	129	4	US-10-425-115-357518	Sequence 357518,
31	33	94.3	138	4	US-10-160-232-86	Sequence 86, Appl
32	33	94.3	138	4	US-10-160-232-90	Sequence 90, Appl
33	33	94.3	227	4	US-10-282-122A-64263	Sequence 64263, A
34	33	94.3	229	4	US-10-425-115-344695	Sequence 344695,
35	33	94.3	257	5	US-10-450-763-43035	Sequence 43035, A
36	33	94.3	296	4	US-10-156-761-9632	Sequence 9632, Ap
37	33	94.3	296	4	US-10-369-493-19811	Sequence 19811, A
38	33	94.3	466	4	US-10-369-493-16537	Sequence 16537, A
39	33	94.3	467	4	US-10-437-963-199114	Sequence 199114,
40	33	94.3	516	4	US-10-450-022-7	Sequence 7, Appli
41	33	94.3	526	4	US-10-450-022-4	Sequence 4, Appli
42	33	94.3	526	4	US-10-450-022-5	Sequence 5, Appli
43	33	94.3	526	5	US-10-450-185B-2	Sequence 2, Appli
44	33	94.3	526	5	US-10-450-185B-17	Sequence 17, Appl
45	33	94.3	526	5	US-10-433-747B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-425-115-308836
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308836
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_44726C.1.pep
US-10-425-115-308836

Query Match	97.1%	Score 34;	DB 4;	Length 58;
Best Local Similarity	57.1%	Pred. No. 1.3e+02;		
Matches	4;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
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Db	49 GYWGASW 55			

RESULT 2
US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036

Query Match 97.1%; Score 34; DB 4; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 34 GYWSSHW 40

RESULT 3
US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited Wells, Jeremy M
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match 97.1%; Score 34; DB 4; Length 452;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 92 GYWLSAW 98

RESULT 4
US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match 97.1%; Score 34; DB 4; Length 466;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 86 GYWVSAW 92

RESULT 5
US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291

Query Match 97.1%; Score 34; DB 4; Length 469;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 97 GYWVASW 103

RESULT 6
US-10-282-122A-66258
; Sequence 66258, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66258
LENGTH: 472
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258
Query Match 97.1%; Score 34; DB 4; Length 472;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 94 GYWISAW 100
RESULT 7
US-10-282-122A-52805
Sequence 52805, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52805
LENGTH: 474
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52805

Query Match 97.1%; Score 34; DB 4; Length 474;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 95 GYWLAW 101

RESULT 8
US-10-369-493-13733
Sequence 13733, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13733
LENGTH: 475
TYPE: PRT
ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733

Query Match 97.1%; Score 34; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYWXXXW 7
Db 93 GYWISAW 99

RESULT 9

US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 57680

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Enterococcus faecium

US-10-282-122A-57680

Query Match

Best Local Similarity 97.1%; Score 34; DB 4; Length 475;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

1 GYWXXXW 7

|||||

95 GYWLSAW 101

RESULT 10

US-10-282-122A-68169

; Sequence 68169, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 68169

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-10-282-122A-68169

Query Match

Best Local Similarity 97.1%; Score 34; DB 4; Length 475;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

1 GYWXXXW 7

|||||

93 GYWISAW 99

RESULT 11

US-10-282-122A-50338

; Sequence 50338, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50338
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Burkholderia mallei
; US-10-282-122A-50338
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Query Match          97.1%; Score 34; DB 4; Length 506;
Best Local Similarity 57.1%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GYWXXXW 7
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Db      124 GYWISAW 130
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RESULT 12
US-09-894-018-87
; Sequence 87, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc..
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
; US-09-894-018-87
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Query Match          97.1%; Score 34; DB 3; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28
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RESULT 13
US-10-474-960A-87
; Sequence 87, Application US/10474960A
; Publication No. US20040248113A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denise
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
; TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby
; FILE REFERENCE: 2060.0320004
; CURRENT APPLICATION NUMBER: US/10/474,960A
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/US02/09877
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/894,018
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-TC
; US-10-474-960A-87
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```

Query Match          97.1%; Score 34; DB 5; Length 585;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 GYWXXXW 7
      |||||
Db      22 GYWQATW 28
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RESULT 14
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
; US-10-046-922-34
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Query Match          94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GYWXXXW 7
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Db ||| |
2 GYWLTIW 8

RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 94.3%; Score 33; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 2 GYWLTIW 8

Search completed: May 2, 2006, 09:32:38
Job time : 75.4186 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 09:26:17 ; Search time 11.3488 Seconds
(without alignments)
32.058 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 35
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
7: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
8: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
9: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
10: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
11: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
12: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	97.1	464	11	US-11-087-099-1003
2	34	97.1	469	11	US-11-087-099-11321
3	34	97.1	471	11	US-11-188-298-19864
4	34	97.1	472	11	US-11-087-099-12291
5	34	97.1	475	11	US-11-087-099-1870
6	34	97.1	475	11	US-11-087-099-2298
7	34	97.1	475	11	US-11-087-099-7571
8	34	97.1	475	11	US-11-188-298-6764
9	34	97.1	476	11	US-11-087-099-1256
10	34	97.1	478	11	US-11-087-099-7019
11	34	97.1	478	11	US-11-087-099-9555
12	34	97.1	478	11	US-11-188-298-8872
13	34	97.1	482	11	US-11-087-099-4146
14	34	97.1	491	11	US-11-087-099-9097
15	33	94.3	119	11	US-11-250-411-97
16	33	94.3	119	11	US-11-250-411-101
17	33	94.3	138	11	US-11-250-411-86
18	33	94.3	138	11	US-11-250-411-90
19	33	94.3	441	11	US-11-087-099-2305
20	33	94.3	456	11	US-11-087-099-8799
21	33	94.3	474	11	US-11-087-099-10672

22	33	94.3	1023	9	US-10-995-561-968	Sequence 968, App
23	32	91.4	122	9	US-10-467-657-5906	Sequence 5906, Ap
24	32	91.4	445	11	US-11-079-463-8428	Sequence 8428, Ap
25	32	91.4	480	11	US-11-079-463-7586	Sequence 7586, Ap
26	32	91.4	566	11	US-11-188-298-3470	Sequence 3470, Ap
27	32	91.4	986	11	US-11-079-463-10025	Sequence 10025, A
28	31	88.6	10	11	US-11-129-741-3641	Sequence 3641, Ap
29	30	85.7	16	9	US-10-929-988-81	Sequence 81, Appl
30	30	85.7	2335	9	US-10-821-234-1610	Sequence 1610, Ap
31	29	82.9	347	9	US-10-506-454-1117	Sequence 1117, Ap
32	29	82.9	400	9	US-10-467-657-7096	Sequence 7096, Ap
33	29	82.9	488	11	US-11-087-099-7125	Sequence 7125, Ap
34	28	80.0	8	11	US-11-045-024-4376	Sequence 4376, Ap
35	28	80.0	8	11	US-11-045-024-4377	Sequence 4377, Ap
36	28	80.0	8	11	US-11-045-024-12720	Sequence 12720, A
37	28	80.0	8	11	US-11-045-024-12755	Sequence 12755, A
38	28	80.0	9	11	US-11-045-024-262	Sequence 262, App
39	28	80.0	9	11	US-11-045-024-263	Sequence 263, App
40	28	80.0	9	11	US-11-045-024-4500	Sequence 4500, Ap
41	28	80.0	9	11	US-11-045-024-4501	Sequence 4501, Ap
42	28	80.0	9	11	US-11-045-024-6570	Sequence 6570, Ap
43	28	80.0	9	11	US-11-045-024-6641	Sequence 6641, Ap
44	28	80.0	10	11	US-11-045-024-2129	Sequence 2129, Ap
45	28	80.0	10	11	US-11-045-024-2130	Sequence 2130, Ap

ALIGNMENTS

RESULT 1
US-11-087-099-1003
; Sequence 1003, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1003
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Oenococcus oeni
US-11-087-099-1003

Query Match 97.1%; Score 34; DB 11; Length 464;
Best Local Similarity 57.1%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
||| |
Db 94 GYWLSSW 100

RESULT 2
US-11-087-099-11321
; Sequence 11321, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11321
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-087-099-11321

Query Match 97.1%; Score 34; DB 11; Length 469;

Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 97 GYWVASW 103

RESULT 3

US-11-188-298-19864
; Sequence 19864, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 19864
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Bacillus cereus ATCC 14579
US-11-188-298-19864

Query Match 97.1%; Score 34; DB 11; Length 471;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 92 GYWLSAW 98

RESULT 4

US-11-087-099-12291
; Sequence 12291, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12291
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-12291

Query Match 97.1%; Score 34; DB 11; Length 472;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 94 GYWISAW 100

RESULT 5

US-11-087-099-1870
; Sequence 1870, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 1870
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas syringae pv. syringae B728a
US-11-087-099-1870

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 93 GYWISAW 99

RESULT 6

US-11-087-099-2298
; Sequence 2298, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2298
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-2298

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 93 GYWISAW 99

RESULT 7

US-11-087-099-7571
; Sequence 7571, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7571
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-087-099-7571

Query Match 97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
|||
Db 93 GYWISAW 99

RESULT 8

US-11-188-298-6764
; Sequence 6764, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.

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; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match          97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 94 GYWLSAW 100

RESULT 9
US-11-087-099-1256
; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1256
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-11-087-099-1256

Query Match          97.1%; Score 34; DB 11; Length 476;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 95 GYWLSAW 101

RESULT 10
US-11-087-099-7019
; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7019
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-7019

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 98 GYWLSAW 104

; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 6764
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Lactobacillus sakei
US-11-188-298-6764

Query Match          97.1%; Score 34; DB 11; Length 475;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 94 GYWLSAW 100

RESULT 9
US-11-087-099-1256
; Sequence 1256, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1256
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Clostridium perfringens
US-11-087-099-1256

Query Match          97.1%; Score 34; DB 11; Length 476;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 95 GYWLSAW 101

RESULT 10
US-11-087-099-7019
; Sequence 7019, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7019
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-11-087-099-7019

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 98 GYWLSAW 104

; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53450)B EP
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9555
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-087-099-9555

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 96 GYWLSAW 102

RESULT 11
US-11-087-099-9555
; Sequence 9555, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9555
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-087-099-9555

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 96 GYWLSAW 102

RESULT 12
US-11-188-298-8872
; Sequence 8872, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8872
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Clostridium perfringens str. 13
US-11-188-298-8872

Query Match          97.1%; Score 34; DB 11; Length 478;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
Db 96 GYWLSAW 102

RESULT 13
US-11-087-099-4146
; Sequence 4146, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4146
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa PAO1
US-11-087-099-4146

Query Match          97.1%; Score 34; DB 11; Length 482;
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Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 94 GYWISAW 100

Db 103 GYWFAYW 109

Search completed: May 2, 2006, 09:33:43
Job time : 11.3488 secs

RESULT 14
US-11-087-099-9097
; Sequence 9097, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9097
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens PfO-1
US-11-087-099-9097

Query Match 97.1%; Score 34; DB 11; Length 491;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
Db 109 GYWISAW 115

RESULT 15
US-11-250-411-97
; Sequence 97, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-97

Query Match 94.3%; Score 33; DB 11; Length 119;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7